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IGNOU MSc ZOOLOGY

PREVIOUS YEAR QUESTIONS (PYQs)

DECEMBER 2025 TERM END EXAMINATION

WITH ODISHA CBZ ZONE

ODISHA
CBZ ZONE

TERM END EXAMINATION (TEE): DEC 2025
SUBJECT: ZOOLOGY (MSC)

No. of Printed Pages : 3 **MZO–004**

M. SC. (ZOOLOGY)

(MSCZOO)

Term-End Examination

December, 2025

MZO-004 : SYSTEMATICS, BIODIVERSITY AND EVOLUTION

Time : 2 Hours *Maximum Marks : 50*

Note : *Attempt any **five** questions. All questions carry equal marks.*

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1. (a) Discuss the trends of evolution in the Post-Darwinism era. 5

   (b) Discuss the role of horizontal gene transfer in evolution. 5

2. Describe the RNA world hypothesis with the help of a well labelled diagram. 10

3. (a) Write the differences between molecular drive and molecular divergence. 4

   (b) How can 16S *r*-RNA gene sequence be used for the construction of the phylogenetic tree ? Explain. 6

4. Write short notes on the following : 5×2=10

   (a) Divergence of transcription system in bacteria and archaea

   (b) Role of transposable elements in bacterial evolution

5. (a) What is genetic drift ? Mention its significance in evolution. 5

   (b) Justify the significance of *Gemmata* sp. and *Giardia* sp. as a connecting link between prokaryotes and eukaryotes. 5

6. (a) How does alpha taxonomy differ from beta and gamma taxonomy ? 3

   (b) Discuss the different theories of biological classification. 7

7. Describe the following : 5×2=10

   (a) Trends in general morphology during human evolution

   (b) Secondary and tertiary endosymbiosis

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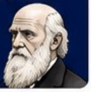
TRENDS OF EVOLUTION IN THE POST-DARWINISM ERA

After Darwin (1859), evolution was viewed through new lenses.

The Post-Darwinian era expanded, tested, and integrated evolutionary theory with genetics, paleontology, ecology and molecular biology.



1. BACKGROUND

Darwin's theory of Natural Selection explained how species change over time.

Post-Darwinian scientists added new ideas, evidence and mechanisms.

Key Shift: From "How does evolution occur?" to "What causes, directs and shapes evolution?"

2. MAJOR TRENDS IN THE POST-DARWINISM ERA

1. Neo-Darwinism (Modern Synthesis)

Darwin + Mendel
Population genetics
Quantitative genetics
Mutation & recombination
Natural selection
= Evolution

(1930s – 1940s)

2. Mutationism

Sudden large mutations are major drivers of evolution.
(De Vries, 1901)

Discontinuous view of evolution.

3. Orthogenesis

Evolution follows an internal, directed trend toward progress.
(Cope, 1896)

Directed evolution.

4. Punctuated Equilibrium

Long periods of stasis (no change) punctuated by brief episodes of rapid change.

(Eldredge & Gould, 1972)

5. Neutral Theory of Molecular Evolution

Most molecular changes are selectively neutral and driven by genetic drift.
(Motoo Kimura, 1968)

3. CHRONOLOGICAL OVERVIEW

1859	Darwin publishes *On the Origin of Species*
1866	Mendel's laws rediscovered
1901–1903	Mutationism proposed (De Vries)
1918	Population genetics starts (Fisher, Haldane, Wright)
1930s–1940s	Modern Synthesis (Neo-Darwinism) takes shape
1950s–1960s	Molecular biology enters evolutionary studies
1960s–Present	Newer syntheses: neutral theory, punctuated equilibrium, extended evo-devo, molecular evolution

4. DETAILED NOTES ON MAJOR TRENDS

Trend	Key Idea	Key Proponents	Highlights / Contributions	Limitations
1. Neo-Darwinism (Modern Synthesis)	Evolution is change in allele frequencies in populations due to natural selection, mutation, genetic drift, migration and recombination.	Fisher, Haldane, Wright, Dobzhansky, Mayr, Simpson, Stebbins	• Combined Darwin's natural selection with Mendelian genetics. • Population is unit of evolution. • Explained adaptation, speciation and diversity. • Strong mathematical & statistical foundation.	• Focus on small-scale changes. • Limited explanation for macroevolutionary patterns initially.
2. Mutationism	Large mutations suddenly produce new species.	Hugo de Vries	• Highlighted the role of mutations. • Basis for mutation breeding in agriculture.	• Overemphasized mutations. • Ignored natural selection.
3. Orthogenesis	Evolution has an inherent direction toward higher complexity.	E. D. Cope	• Emphasized internal factors (vital force) and trends. • Explained linear series in fossils.	• No experimental evidence. • Rejected by Modern Synthesis.
4. Punctuated Equilibrium	Evolution occurs in short bursts; long periods of stability in between.	Niles Eldredge & Stephen Jay Gould	• Based on fossil record. • Explains rapid speciation events. • Compatible with Modern Synthesis (e.g., peripatric speciation).	• Not universal. • Mechanisms still under study.
5. Neutral Theory of Molecular Evolution	Most genetic changes at molecular level are neutral and fixed by genetic drift.	Motoo Kimura	• Explains molecular variation. • Introduced molecular clock concept. • Supported by DNA sequence data.	• Does not explain adaptive changes. • Neutral ≠ no function always.

5. OTHER IMPORTANT TRENDS

Molecular Evolution
Use of molecular data (DNA, RNA, proteins) to understand evolution.

Evolutionary Developmental Biology (Evo-devo)
Studies how changes in development cause evolutionary changes.

Niche Construction
Organisms modify their environment and shape their own evolution (e.g., beavers, earthworms).

Extended Evolutionary Synthesis (EES)
Integrates genetics, epigenetics, ecology, devolopment, niche construction and culture.

6. COMPARATIVE SNAPSHOT

Feature	Neo-Darwinism	Mutationism	Orthogenesis	Punctuated Equilibrium	Neutral Theory
Nature of Change	Gradual, small changes in populations	Sudden, large mutations	Gradual, directed	Sudden bursts + long stasis	Mostly neutral molecular changes
Direction	Non-directional (adaptive)	Non-directional	Directed (toward progress)	No overall direction	No overall direction
Main Force	Natural selection + genetics	Mutations	Internal factors (vital force)	Speciation events	Genetic drift
Level	Population	Species	Lineages	Species / lineages	Molecular level
Status Today	Widely accepted (modern basis)	Limited role	Largely rejected	Supported with modifications	Well supported for molecular evolution

7. SIGNIFICANCE

- ✓ Provided a more complete understanding of evolution.
- ✓ Integrated genetics, paleontology, ecology and molecular biology.
- ✓ Helped explain patterns at all levels—from molecules to ecosystems.
- ✓ Forms the foundation of modern evolutionary biology.

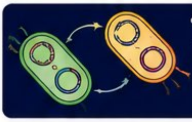
8. KEY TAKEAWAY

Post-Darwinism expanded evolution from a single mechanism (natural selection) to a multi-factorial, evidence-based, and integrative science, leading to the modern evolutionary synthesis and beyond.

MNEMONIC TO REMEMBER TRENDS

"Nice Mutations Often Produce New Data"

N	M	O	P	N
Neo-Darwinism	Mutationism	Orthogenesis	Punctuated Equilibrium	Neutral Theory



THE ROLE OF HORIZONTAL GENE TRANSFER (HGT) IN EVOLUTION

Genes can move across species and reshape life's history.

HGT is a powerful engine of evolutionary innovation.

1. WHAT IS HORIZONTAL GENE TRANSFER?

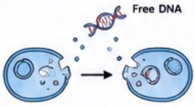
- Horizontal Gene Transfer (HGT) is the movement of genetic material between organisms other than by inheritance from parent to offspring.
- It is common in prokaryotes and also occurs in eukaryotes (plants, fungi, and animals).
- It allows organisms to acquire new genes rapidly, providing instant adaptive advantages.

HGT = Sharing genes sideways, not vertically from parents.

2. MAIN MECHANISMS OF HORIZONTAL GENE TRANSFER

1. Transformation

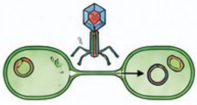
Uptake of free (naked) DNA from the environment by a competent cell.



Example: *Streptococcus pneumoniae* acquires antibiotic resistance genes.

2. Transduction

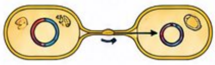
Transfer of DNA mediated by bacteriophages (viruses that infect bacteria).



Example: Phage carrying toxin genes from one bacterium to another.

3. Conjugation

Direct transfer of DNA (usually plasmids) between cells through cell-to-cell contact (pili).



Example: Transfer of antibiotic resistance plasmids in *E. coli*.

3. HOW HGT DRIVES EVOLUTION

Rapid acquisition of new traits
Genes for new functions (e.g., antibiotic resistance, metabolism) are gained instantly without waiting for slow mutations.

Increases genetic diversity
Introduces novel genes and alleles into populations and across species.

Adaptation to new environments
Helps organisms survive stress, toxins, new niches and changing conditions.

Creates new gene combinations
Transferred genes can recombine with existing genes and evolve new functions.

Can accelerate speciation
Gene transfer across lineages may lead to new traits that promote reproductive isolation and lineage diversification.

4. EXAMPLES OF HGT AND THEIR EVOLUTIONARY IMPACT

Example	Organisms Involved	Transferred Gene(s)	Evolutionary Impact
Antibiotic resistance	Bacteria (e.g., *E. coli*, Staphylococcus)	Genes encoding resistance enzymes (e.g., β-lactamase)	Rapid spread of antibiotic resistance worldwide.
Nitrogen fixation	Rhizobium bacteria ↔ Legume plants	nit genes from soil bacteria/plasmids	Enabled legumes to colonize nitrogen-poor soils; major ecological success.
Photosynthesis genes	Cyanobacteria → Eukaryotic algae (and plants)	*psbA* (D1 protein of photosystem II)	Key gene transfer event that contributed to the evolution of oxygenic photosynthesis in eukaryotes.
Cellulose degradation	Bacteria → Fungi	Genes for cellulases and hemicellulases	Helped fungi evolve the ability to decompose plant biomass and diversify niches.
Placental development (Endogenous retroviruses)	Viruses → Mammals	*syncytin* (from retroviral envelope genes)	Important for placental fusion and development in mammals.
Thermophily in bacteria	Bacteria in extreme hot environments	Genes for heat-shock proteins and DNA repair	Improved survival in extreme conditions; niche expansion.

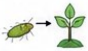
5. HGT IN EUKARYOTES

- Occurs in plants, fungi, protists and animals, though less frequent than in bacteria.
- Often mediated by: parasites, viruses, symbiotic relationships, or endosymbiosis.
- Plays important roles in adaptation, development and immune defense.

Examples in Eukaryotes

Aphid → Plant

Aphids transfer genes to plants that help resist aphid feeding.

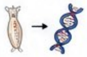


Fungi ↔ Plants

Gene transfer between fungi and poplars affects wood decomposition.

Bdelloid Rotifers

Acquire genes from fungi, bacteria, and plants and animals.



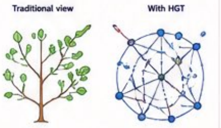
6. HGT vs VERTICAL GENE TRANSFER

Feature	Vertical Gene Transfer (Inheritance)	Horizontal Gene Transfer
Direction	Parent → Offspring	Between unrelated individuals/species
Speed	Slow (via mutations and selection)	Fast (instant acquisition)
Genetic Scope	Within a lineage	Across lineages/ species
Role	Maintains existing information	Introduces new information
Importance	Stability	Innovation and adaptation

7. SIGNIFICANCE OF HGT IN EVOLUTION

- Expands the gene pool beyond reproduction.
- Helps organisms survive antibiotics, toxins, viruses and harsh environments.
- Drives evolution of new metabolic pathways and complex traits.
- Influences the origin of organelles (e.g., chloroplasts and mitochondria via ancient endosymbiosis – a form of HGT).
- Challenges the traditional "tree of life" model and supports a "web of life".

TREE OF LIFE vs WEB OF LIFE



HGT connects distant branches.

8. LIMITATIONS AND CONSIDERATIONS

- Not all transferred genes are retained; selection determines their fate.
- HGT is more common in microbes; rarer in multicellular organisms.
- Detection can be difficult; needs genomic, phylogenetic and ecological evidence.

Evidence for HGT

- GC content differences
- Phylogenetic incongruence
- Presence of mobile elements (plasmids, transposons)
- Gene context and function
- Experimental transfer studies

9. KEY TAKEAWAY

Horizontal gene transfer is a major evolutionary force that moves genes across the boundaries of species and lineages. It generates genetic novelty, promotes adaptation, and has profoundly shaped the diversity of life on Earth.

MNEMONIC TO REMEMBER MECHANISMS

"TTC – Take The Genes"

T – Transformation (naked DNA uptake)
T – Transduction (phage-mediated)
C – Conjugation (cell contact)

In short: HGT provides nature with shortcuts to innovation. It is a powerful process that shapes genomes, drives adaptation and empowers life to thrive in a constantly changing world.

THE RNA WORLD HYPOTHESIS

The earliest life was based on RNA, not DNA or proteins.

Proposed by Carl Woese (1967)

1. WHAT IS RNA WORLD HYPOTHESIS?

- It proposes that early life on Earth was based on RNA.
- RNA was the first genetic material and also acted as a catalyst.
- Later, DNA evolved for more stable storage of genetic information and proteins evolved for diverse functions.
- Thus, life evolved from an RNA-based system to the DNA–protein world.

In short:
RNA came first → DNA came later → Proteins came last.

2. WHY RNA COULD HAVE COME FIRST?

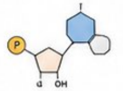
a) Genetic Material

RNA can store genetic information.

b) Catalytic Activity

Some RNAs (ribozymes) can catalyse chemical reactions.

c) Simpler Structure



Built from four ribonucleotides; easier to synthesize prebiotically.

d) Versatility

One molecule can both store information and catalyse reactions.

e) Evolutionary Advantage

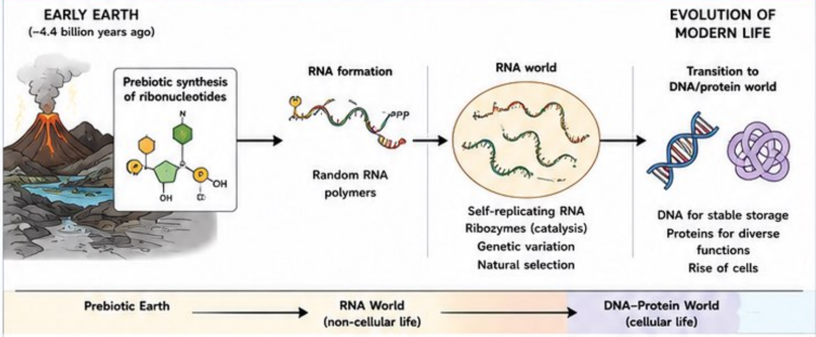
RNA systems could evolve faster and adapt in early Earth conditions.

Key Idea:
RNA is a "genetic catalyst"; it can replicate itself and speed up chemical reactions necessary for life.

3. MAIN FEATURES OF RNA WORLD

- **Self-replication:** RNA molecules could make copies of themselves.
- **Catalysis:** RNA (ribozymes) could catalyse formation of phosphodiester bonds and other reactions.
- **Genetic diversity:** Mutations in RNA created variation; natural selection acted on RNA populations.
- **Non-cellular life:** Life existed as RNA networks or "RNA pools" without cells.
- **Pre-dates DNA and proteins:** DNA and proteins evolved later to improve fidelity and expand functions.

4. DIAGRAMMATIC REPRESENTATION OF RNA WORLD HYPOTHESIS



EARLY EARTH
(~4.4 billion years ago)

Prebiotic synthesis of ribonucleotides

RNA formation

Random RNA polymers

RNA world

Self-replicating RNA
Ribozymes (catalysis)
Genetic variation
Natural selection

EVOLUTION OF MODERN LIFE

Transition to DNA/protein world

DNA for stable storage
Proteins for diverse functions
Rise of cells

Prebiotic Earth → RNA World (non-cellular life) → DNA–Protein World (cellular life)

According to the hypothesis, life evolved in stages from simple RNA molecules to complex cellular organisms.

5. EVIDENCES IN SUPPORT

- ✓ **Ribozymes exist:** e.g., RNA can act as enzymes (peptidyl transferase activity in ribosome).
- ✓ **Ribosome core is ribozyme:** Peptidyl transferase activity is performed by rRNA, not protein.
- ✓ **RNA can replicate:** In vitro selection of RNA molecules with replicase activity.
- ✓ **Universality of genetic code:** Suggests early RNA world with simple coding systems.
- ✓ **Prebiotic synthesis possible:** Experiments show ribonucleotides can form under simulated early Earth conditions.
- ✓ **RNA viruses:** Many viruses use RNA genomes, indicating ancient origin.

6. MAJOR TRANSITIONS (FROM RNA WORLD TO MODERN LIFE)

1. RNA replication became more efficient.
2. DNA evolved from RNA (more stable, double-stranded).
3. Proteins evolved (from simple peptides) for structural and catalytic diversity.
4. Ribozymes were gradually replaced by protein enzymes (more efficient).
5. Cellular compartmentalization evolved (membranes, metabolism).
6. Modern cells with DNA, RNA and proteins appeared.

Thus, RNA world → RNP world → DNA–Protein world → Cellular life
(RNP = ribonucleoprotein world)

7. SIGNIFICANCE

- Provides a plausible explanation for the origin of life.
- Explains how information storage and catalysis could have evolved together.
- Links the chemistry of prebiotic Earth to the biology of modern cells.
- Supported by modern discoveries of ribozymes, RNA viruses and the central role of rRNA in ribosomes.

8. KEY POINTS TO REMEMBER

- RNA was the first genetic material and catalyst.
- RNA could self-replicate and evolve.
- DNA and proteins evolved later for stability and diversity.
- Life evolved from a non-cellular RNA world to cellular life.
- RNA world hypothesis bridges chemistry and biology in the origin of life.

9. LIMITATIONS / CHALLENGES

- ⚠ RNA is chemically unstable (2'-OH group makes it prone to hydrolysis).
- ⚠ Self-replication of RNA is not yet fully efficient.
- ⚠ Prebiotic synthesis of large RNA polymers is difficult.
- ⚠ Transition from RNA world to DNA–protein world is not completely understood.

10. SUMMARY FLOW

Prebiotic synthesis of ribonucleotides
↓
Formation of RNA polymers
↓
RNA world (replication + catalysis)
↓
Evolution of DNA and proteins
↓
Modern cellular life

CONCLUSION: The RNA world hypothesis is a pioneering idea that suggests life began with RNA molecules capable of storing information and catalysing reactions. It laid the foundation for the evolution of DNA, proteins and eventually all living organisms.

IGNOU PG (MZO-04)
EXAM PREPARATION

QUESTION 4 (a & b) – SHORT NOTES

5 × 2 = 10 MARKS

A DIVERGENCE OF TRANSCRIPTION SYSTEM IN BACTERIA AND ARCHAEA

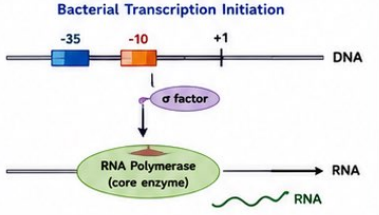
KEY POINTS

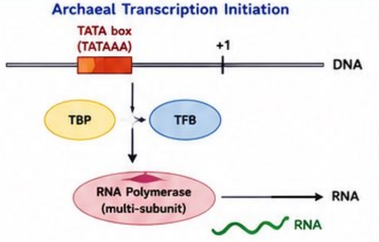
- ✓ Both bacteria and archaea transcribe DNA to RNA but their transcription machineries are fundamentally different.
- ✓ Bacteria have a simpler system with one type of RNA polymerase.
- ✓ Archaea possess a more complex system, closer to eukaryotes.
- ✓ Differences reflect their evolutionary divergence.

COMPARATIVE OVERVIEW

Feature	Bacteria	Archaea
RNA Polymerases	One type (RNA polymerase core enzyme with σ factor)	Three main types (RNA polymerase I, II, III) + multiple subunits
Core Enzyme Structure	$\alpha_2 \beta \beta' \omega$	Complex multi-subunit (8–14 subunits)
Sigma Factors	Many σ factors (σ70, σ32, σ54, etc.)	TATA-binding protein (TBP) + Transcription factors (TFB) instead of σ factors
Promoter Elements	-35 and -10 (Pribnow box) recognized by σ factor	TATA box (usually TATAAA) recognized by TBP
Initiation Mechanism	σ factor binds promoter → recruits RNAP → open complex	TBP binds TATA box → TFB + RNAP assembly → open complex
Similarity to Eukaryotes	Low	High (similar RNAP structure and initiation factors)

DIAGRAMMATIC COMPARISON


Bacterial Transcription Initiation


Archaeal Transcription Initiation

SIGNIFICANCE

- Shows evolutionary distance: bacteria (simple) → archaea (complex, eukaryote-like).
- Archaeal transcription system supports their placement closer to eukaryotes.
- Important for understanding gene regulation and evolution of transcription machinery.

B ROLE OF TRANSPOSABLE ELEMENTS IN BACTERIAL EVOLUTION

KEY POINTS

- ✓ Transposable elements (TEs) are DNA sequences that can move within the genome.
- ✓ They are major drivers of bacterial genome organization, diversity and evolution.
- ✓ TEs include insertion sequences (IS), transposons, integrons and prophages.
- ✓ They create variation, promote adaptation and shape genome architecture.

MAJOR CONTRIBUTIONS OF TEs

1. Generation of Genetic Variation
- Insertion, deletion and rearrangement of genes.
- Creates new mutations and gene combinations.

2. Gene Acquisition and Transfer
- Carry genes like antibiotic resistance, virulence, metabolic genes.
- Facilitate horizontal gene transfer.

3. Genome Plasticity
- Cause genome rearrangements (inversions, duplications, deletions).
- Lead to genome expansion or reduction.

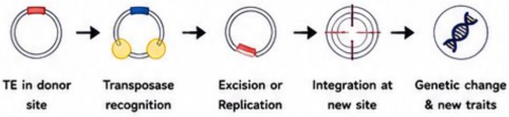
4. Regulation of Gene Expression
- Insertion near promoters can upregulate or downregulate genes.
- Provide new promoters or terminators.

5. Adaptation and Evolution
- Help bacteria adapt to new environments, stress, antibiotics.
- Drive rapid evolution of bacterial populations.

TYPES OF TRANSPOSABLE ELEMENTS IN BACTERIA

Type	Key Feature	Example
Insertion Sequences (IS)	Simplest TEs; contain only transposase gene.	IS1, IS10
Composite Transposon	Two IS elements flank additional genes.	Tn5
Transposons	Carry other genes (e.g., resistance genes).	Tn3, Tn21
Integrons	Capture gene cassettes by site-specific recombination.	Class 1 integron
Prophages (Phage elements)	Bacteriophages can integrate and carry genes.	Lambda prophage

MECHANISM OF ACTION (SIMPLIFIED)



SIGNIFICANCE

- TEs are powerful agents of genomic innovation.
- They contribute to emergence of new species, antibiotic resistance and pathogenicity.
- Key players in shaping bacterial genome evolution and adaptability.

EXAM TIP (2 MARKS ANSWER)

- Define TEs briefly.
- List 2–3 major roles.
- Give examples (e.g., IS elements, transposons, integrons).

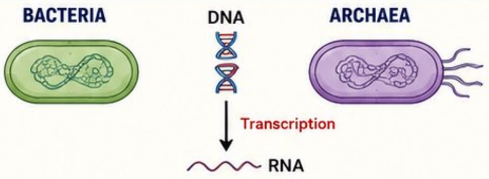
SHORT NOTE STRATEGY: Write crisp points, use tables/diagrams, give examples.

1(a) DIVERGENCE OF TRANSCRIPTION SYSTEM IN BACTERIA AND ARCHAEA

OVERVIEW

Transcription is the first step of gene expression in which DNA is transcribed into RNA by **RNA polymerase (RNAP)**.

Bacteria and Archaea have both similarities and significant differences in their transcription systems.



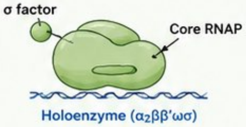
COMPARISON AT A GLANCE

Feature	Bacteria	Archaea
RNA Polymerase	Single type of RNAP	Multiple RNAPs similar to eukaryotes (RNAP I, II, III)
Subunit Composition	Core enzyme: $\alpha_2\beta\beta'\omega$ (4–5 subunits)	More complex: 10–14 subunits (similar to eukaryotic RNAP II)
Promoter Recognition	−35 (TTGACA) and −10 (TATAAT) elements recognized by σ factor	TATA box (−25 to −30 region) recognized by TBP/TAF
σ Factor / Transcription Factors	σ factor essential for promoter recognition and initiation	σ factor absent Uses TBP and other general factors
Initiation Mechanism	σ factor binds to core RNAP → forms holoenzyme → promoter melting and initiation	TBP binds TATA box → recruits RNAP and other factors → initiates transcription
Termination	Rho-dependent and Rho-independent	Rho-like proteins present; mechanism similar to eukaryotes
Similarity with Eukaryotes	Low	High (especially in RNAP structure, promoters and transcription factors)

BACTERIAL TRANSCRIPTION SYSTEM

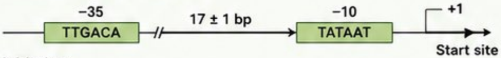
① Components

- Core RNA polymerase: $\alpha_2\beta\beta'\omega$
- σ factor (sigma factor)



② Promoter Structure

- −35 (TTGACA) and −10 (TATAAT) elements upstream of +1 site



③ Initiation

σ factor binds promoter → recruits core RNAP → open complex formation → RNA synthesis starts.

④ Elongation

RNAP moves along DNA template synthesizing RNA 5′ → 3′.

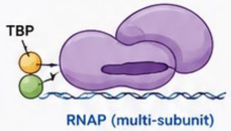
⑤ Termination

Rho-dependent (uses Rho protein) or
Rho-independent (hairpin structure + U-rich sequence).

ARCHAEAL TRANSCRIPTION SYSTEM

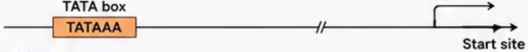
① Components

- Multiple RNA polymerases: RNAP I, RNAP II, RNAP III
- General transcription factors: TBP, TFB, TFE, etc.



② Promoter Structure

- **TATA box** (TATAAA) located ~25 to −30 upstream of +1 site.



③ Initiation

TBP binds TATA box → recruits RNAP and other factors → open complex formation → RNA synthesis starts.

④ Elongation

Similar to eukaryotes; processive and efficient.

⑤ Termination

Uses Rho-like proteins and intrinsic terminators; mechanism more eukaryote-like.

KEY POINTS

- ✓ Bacteria use σ factor and simple RNAP (4–5 subunits).
- ✓ Archaea lack σ factor; use TBP and multiple RNAPs similar to eukaryotes.
- ✓ Archaeal promoters have TATA box; bacteria have −35 and −10 elements.
- ✓ Archaea show greater similarity to eukaryotic transcription machinery.

SIGNIFICANCE

- ✓ Understanding these differences helps in studying evolution of transcription machinery.
- ✓ Important for biotechnology, drug target identificators and understanding gene regulation in extremophiles.

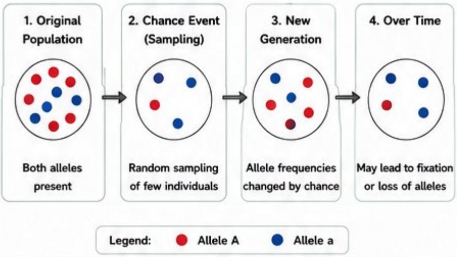
5 (a)

WHAT IS GENETIC DRIFT?
ITS SIGNIFICANCE IN EVOLUTION

WHAT IS GENETIC DRIFT?

- Genetic drift refers to random changes in allele frequencies in a population due to chance events.
- It is non-adaptive and occurs independent of natural selection.
- Its effect is strongest in small populations.

HOW GENETIC DRIFT WORKS?



1. Original Population – Both alleles present

2. Chance Event (Sampling) – Random sampling of few individuals

3. New Generation – Allele frequencies changed by chance

4. Over Time – May lead to fixation or loss of alleles

Legend: ● Allele A ● Allele a

KEY FEATURES

- ➤ Random process
- ➤ Non-directional
- ➤ Alters allele frequencies
- ➤ Can lead to loss of genetic variation
- ➤ More effective in small populations

TYPES OF GENETIC DRIFT

◆ **Founder Effect**

New population established by few individuals; different allele frequencies from original population.

◆ **Bottleneck Effect**

Sudden reduction in population size due to events like natural disasters; survivors carry only a subset of alleles.

SIGNIFICANCE IN EVOLUTION

- ✓ Can cause fixation of new alleles and loss of others.
- ✓ Leads to genetic variation — raw material for evolution.
- ✓ Important in small, isolated populations (e.g., islands).
- ✓ May cause divergence between populations.
- ✓ Aids in speciation when combined with isolation.
- ✓ Helps in the elimination of deleterious alleles (by chance) sometimes.

EXAM POINTERS (2–5 MARKS)

- Define genetic drift.
- Types: Founder effect & Bottleneck effect.
- Features: random, non–adaptive, alters allele frequencies.
- Significance: source of variation, causes divergence, important in evolution.

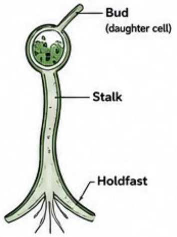
IN SHORT: Genetic drift is a random change in allele frequencies due to chance. It is powerful in small populations and plays an important role in evolution by creating variation, causing divergence and contributing to speciation.

---

5 (b)

SIGNIFICANCE OF GEMMATA SP. AND GIARDIA SP.
AS A CONNECTING LINK BETWEEN PROKARYOTES AND EUKARYOTES

GEMMATA SP.
(A Budding Bacterium)

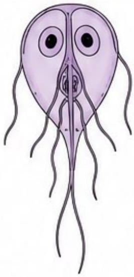


- ◆ Unicellular, freshwater bacterium.
- ◆ Reproduces by budding.
- ◆ Forms a stalk and holdfast like lower eukaryotes.
- ◆ Lacks true nucleus and membrane–bound organelles.
- ◆ Possesses a peptidoglycan cell wall (bacterial trait).

SIMILARITIES WITH EUKARYOTES

- Budding reproduction (asexual)
- ↔ Presence of stalk/ attachment structure ↔
- ↔ Complex cell organization ↔
- ↔ Multiple chromosomes (in some strains) ↔
- ↔ Membrane–bound mesosomes ↔
- ↔ More complex than typical bacteria ↔
- ↔ Resemblance to primitive eukaryotic ancestors ↔

GIARDIA SP.
(A Flagellated Protozoan)



- ◆ Unicellular, parasitic protozoan (found in small intestine).
- ◆ Bilateral symmetry.
- ◆ Two nuclei (eukaryotic feature).
- ◆ Possesses flagella for locomotion.
- ◆ Lacks mitochondria, Golgi apparatus and true cytostome.
- ◆ Anaerobic metabolism (uses hydrogenosomes).
- ◆ Nuclei show prokaryotic type histones (in some species).

WHY CONNECTING LINK?

- ✓ These organisms show characters intermediate between prokaryotes and eukaryotes.
- ✓ Both are more advanced than bacteria but lack many typical eukaryotic features.
- ✓ They help in understanding the evolutionary transition from simple prokaryotic ancestors to complex eukaryotes.
- ✓ Provide evidence for gradual evolution.

KEY DIFFERENCES (FROM TYPICAL EUKARYOTES)

Feature	Gemmata sp.	Giardia sp.	Typical Eukaryotes
Nucleus	Absent (nucleoid)	Present (2 nuclei)	Present (true nucleus)
Membrane–bound organelles	Absent	Few / reduced (e.g., no mito., Golgi)	Many (mitochondria, ER, Golgi, lysosomes)
Cell wall	Present (peptidoglycan)	Absent	Absent (in animals)
Mode of nutrition	Autotrophic?	Parasitic (anaerobic)	Autotrophic / Heterotrophic

EXAM TIP (5 MARKS ANSWER)

- Define both organisms briefly.
- Mention key features.
- Highlight similarities with eukaryotes.
- Conclude why they are connecting links.

IN SHORT

Gemmata sp. (bacterium with budding) and Giardia sp. (primitive protozoan) possess a mix of prokaryotic and eukaryotic characters. They represent intermediate forms and act as connecting links in evolution.

5 MARKS

(a) HOW DOES ALPHA TAXONOMY DIFFER FROM BETA AND GAMMA TAXONOMY?

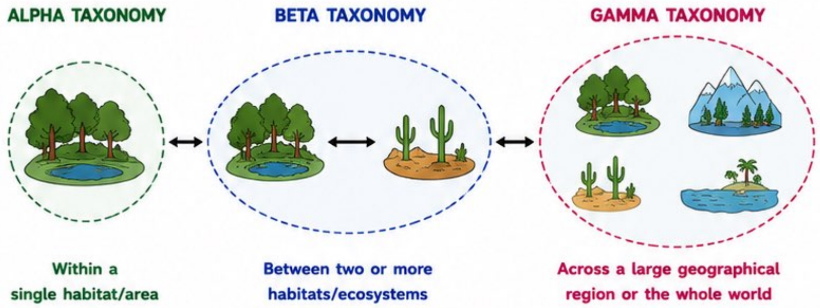
IGNOU MZO-04

DEFINITION

Taxonomy is the science of identification, description, naming and classification of organisms.

- **Alpha taxonomy** – study of diversity within a particular area or habitat.
- **Beta taxonomy** – study of diversity between habitats or ecosystems.
- **Gamma taxonomy** – study of total diversity at large geographical scale.

CONCEPTUAL DIAGRAM – LEVELS OF TAXONOMIC SCOPE



ALPHA TAXONOMY

Within a single habitat/area

BETA TAXONOMY

Between two or more habitats/ecosystems

GAMMA TAXONOMY

Across a large geographical region or the whole world

KEY DIFFERENCES BETWEEN ALPHA, BETA AND GAMMA TAXONOMY

Basis	ALPHA TAXONOMY	BETA TAXONOMY	GAMMA TAXONOMY
Focus	Diversity within a particular habitat or area.	Diversity between habitats or ecosystems.	Total diversity over a large geographical area.
Spatial Scale	Local scale (small area).	Regional scale (between areas).	Global scale (continent, biome or entire world).
Purpose	To determine the number of species present in a specific area.	To compare species composition between different areas.	To assess overall richness of species on Earth.
Type of Diversity	Intra-habitat diversity (within habitat).	Inter-habitat diversity (between habitats).	Total or landscape diversity.
Measurement	Species richness and abundance in one site.	Species turnover (similarity/dissimilarity) between sites.	Total species richness at large scale.
Example / Application	Flora and fauna of a pond, forest patch or field.	Comparison of species between forest and grassland.	Study of biodiversity of India or the whole Earth.

IMPORTANT POINTS

- ✓ Alpha < Beta < Gamma in terms of increase in spatial scale.
- ✓ Alpha deals with local diversity.
- ✓ Beta measures change in species composition.
- ✓ Gamma represents total diversity at the largest scale.

EXAM POINTS (3 MARKS)

- ★ Define alpha, beta and gamma taxonomy.
- ★ Write the basis of their differences.
- ★ Prepare a comparison table.
- ★ Give one example for each.

FOCUS KEYWORDS:
Within – Between – Total
Local – Regional – Global

IN SHORT

Alpha studies diversity within an area, Beta compares diversity between areas, and Gamma studies total diversity over large geographical scale.

REMEMBER: **Alpha** (Inside) – **Beta** (Between) – **Gamma** (Global)

5 (b) THEORIES OF BIOLOGICAL CLASSIFICATION

IGNOU
MZO-04

Biological classification is based on different principles and has evolved through several theories.

INTRODUCTION

- Classification arranges organisms into groups based on similarities and differences.
- Different theories have been proposed at different times based on available knowledge and methods.
- These theories reflect our understanding of relationships among organisms.

MAIN THEORIES OF BIOLOGICAL CLASSIFICATION

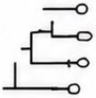
1 Artificial System

Based on one or two easily observable characters.

2 Natural System

Based on many characters reflecting natural relationships.

3 Phylogenetic System

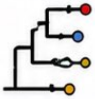


Based on evolutionary relationships and ancestry.

4 Numerical (Phenetic) System

Based on overall similarity using numerical data and statistics.

5 Cladistic System



Based on shared derived characters (cladistics).

COMPARISON OF DIFFERENT THEORIES

Feature	Artificial	Natural	Phylogenetic	Numerical (Phenetic)	Cladistic
Basis	One or few superficial characters	Many characters (morphological, anatomical)	Evolutionary relationships (phylogeny)	Overall similarity (numerical analysis)	Common derived characters (synapomorphies)
Approach	Subjective	Comparative and holistic	Historical and evolutionary	Objective and quantitative	Objective and evolutionary
Data Used	Few, easily seen characters	Many types of characters	Fossils, morphology, embryology, molecules	Many characters coded as numbers	Morphological, molecular characters
Merits	Simple and easy to use	More natural and reliable	Shows actual evolutionary relationships	Reduces subjectivity; statistically testable	Most natural; reflects true evolutionary patterns
Demerits	Unnatural; many unrelated groups	Does not show evolutionary relationships	Difficult due to incomplete fossil record	Ignores evolutionary history	Requires detailed data; complex analysis
Key Proponent	Linnaeus	J.S. Hutton, de Jussieu	Haeckel, Engler & Prantl	Sokal, Sneath	Hennig

BRIEF EXPLANATION OF EACH THEORY

1. **Artificial System:** Earliest system. Groups organisms using one or two easily observable characters (e.g., habit, habitat, color).
2. **Natural System:** Uses many characters to classify organisms. Attempts to reflect natural relationships.
3. **Phylogenetic System:** Arranges organisms in the sequence of their evolution. Emphasizes ancestry and descent.
4. **Numerical (Phenetic) System:** Uses numerical data and statistical methods to classify organisms based on overall similarity.
5. **Cladistic System:** Groups organisms based on common derived characters and constructs cladograms showing evolutionary branching.

SIGNIFICANCE OF THESE THEORIES

- ✓ Helped in understanding diversity and relationships.
- ✓ Provided a framework for modern classification.
- ✓ Phylogenetic and cladistic approaches reflect evolutionary history.
- ✓ Basis for modern systems like molecular classification.

EXAM POINTS (5 MARKS)

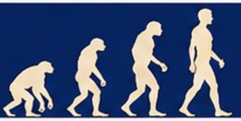
- ★ Define theories of biological classification.
- ★ Write features of any two theories.
- ★ Compare any two theories.
- ★ Explain significance of these theories.

IN SHORT

Theories of classification differ in the basis and approach used, but all aim to arrange organisms into natural and meaningful groups.

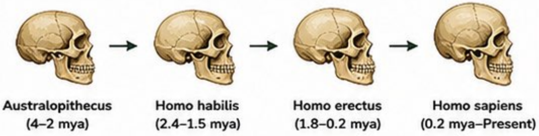
★ **REMEMBER:** Artificial – Simple | Natural – Many Characters | Phylogenetic – Evolution | Numerical – Similarity | Cladistic – Common Derived Characters

TRENDS IN GENERAL MORPHOLOGY DURING HUMAN EVOLUTION



Human evolution is marked by gradual morphological changes that reflect adaptation to bipedalism, increasing brain size, complex behavior and culture.

1. SKULL AND DENTITION


Australopithecus (4–2 mya)
Homo habilis (2.4–1.5 mya)
Homo erectus (1.8–0.2 mya)
Homo sapiens (0.2 mya–Present)

Cranial capacity	Increase from ~400–500 cc to ~1300–1500 cc
Forehead	From low and receding to high and vertical
Face	From projecting to flat (orthognathous)
Jaw	From robust to gracile
Teeth	Reduction in size, especially canines and premolars
Chin	Development of mental eminence in modern humans
Brow ridges	Prominent in early humans → reduced in modern humans

2. POSTCRANIAL SKELETON

Vertebral Column
From C-shaped (quadrupedal) to S-shaped (bipedal) for balance and shock absorption

Thorax
From funnel-shaped to barrel-shaped

Pelvis
From long and narrow to short, broad and bowl-shaped

Upper Limbs
From long and curved (climbing) to shorter and freer for manipulation

Lower Limbs
From shorter to longer and stronger

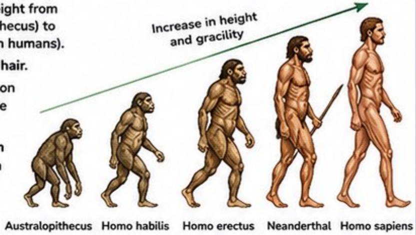
Knee
From less stable to stable with enlarged femoral condyles

Foot
From grasping foot with divergent big toe to arched foot with aligned big toe

Overall
Rigidity and efficiency for upright walking

3. BODY SIZE AND PROPORTIONS

- Increase in body height from ~1.1 m (Australopithecus) to ~1.7–1.8 m (modern humans).
- Reduction in body hair.
- More gracile skeleton and reduced muscle attachments.
- Sexual dimorphism reduced in modern humans.



4. BRAIN AND NEUROCRANIUM

- Steady increase in brain size and complexity.
- Expansion of cerebral vault with rounded cranial shape.
- Reorganization of brain regions responsible for cognition, planning, language and creativity.

Species	Cranial Capacity (cc)
Australopithecus	400 – 500
Homo habilis	600 – 750
Homo erectus	850 – 1100
Neanderthal	1200 – 1600
Homo sapiens (modern)	1300 – 1500

5. TRENDS IN GENERAL MORPHOLOGY – SUMMARY

→ From quadrupedalism to bipedalism
→ From projecting face to flat face
→ From small brain to large brain
→ From heavy jaws and large teeth to light jaws and small teeth
→ From curved spine to S-shaped spine
→ From grasping foot to arched foot
→ From long arms to short arms
→ From robust body to more gracile body

6. SIGNIFICANCE

- Reflects adaptation to upright walking and efficiency.
- Indicates increasing brain function, culture and technology.
- Shows dietary changes and reduction in masticatory stress.
- Provides evidence for evolutionary relationships among hominins.

7. KEY TAKEAWAY

> “Human evolution shows a clear trend from primitive ape-like ancestors to modern humans through gradual morphological changes driven by adaptation, natural selection and lifestyle.

QUICK TIMELINE OF MORPHOLOGICAL TRENDS

Australopithecus (4–2 mya)

- Small brain
- Prognathous face
- Long arms, short legs
- Grasping foot

Homo habilis (2.4–1.5 mya)

- Slightly larger brain
- Reduced jaws and teeth
- More upright posture

Homo erectus (1.8–0.2 mya)

- Larger brain
- Barrel-shaped chest
- Long legs, short arms
- Arched foot

Neanderthal (0.4–0.04 mya)

- Large brain
- Robust body
- Reduced brow ridges

Homo sapiens (0.2 mya–Present)

- Highest brain capacity
- Vertical forehead
- Chin present
- Modern body proportions

SECONDARY & TERTIARY ENDOSYMBIOSIS

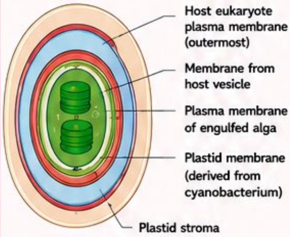
Formation of Complex Plastids by Engulfment of Algae and Algal Eukaryotes

WHAT IS ENDOSYMBIOSIS?

Endosymbiosis is a close and permanent association between two different organisms where one lives inside the other. It explains the origin of plastids in eukaryotic cells.

- ✓ **Primary endosymbiosis:** Engulfment of cyanobacterium → primary plastid (2 membranes).
- ✓ **Secondary & Tertiary endosymbiosis:** Engulfment of algae and algal eukaryotes → complex plastids (3 or more membranes).

MEMBRANE ARRANGEMENT


Host eukaryote plasma membrane (outermost)
Membrane from host vesicle
Plasma membrane of engulfed alga
Plastid membrane (derived from cyanobacterium)
Plastid stroma

Secondary plastids → 3 or 4 membranes

4. EVIDENCE FOR SECONDARY & TERTIARY ENDOSYMBIOSIS

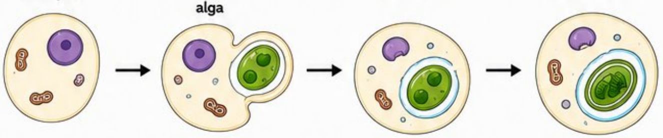
- ✓ Presence of 3 or more membranes around plastids.
- ✓ Presence of nucleomorph in many organisms.
- ✓ Ribosomes in plastids are eukaryotic type (80S).
- ✓ Phylogenetic studies show close relationship between plastids and algal lineage.
- ✓ Endoplasmic reticulum surrounds the plastid.

5. SIGNIFICANCE

- ✓ Explains the origin of diverse plastids.
- ✓ Led to evolution of many photosynthetic protists and algae.
- ✓ Increased complexity and adaptability in aquatic habitats.
- ✓ Demonstrates the power of endosymbiosis in evolution.

1. SECONDARY ENDOSYMBIOSIS

A eukaryotic cell engulfs a photosynthetic alga and retains it as a plastid.



① Heterotrophic eukaryote → ② Engulfment of photosynthetic alga → ③ Alga retained inside host cell → ④ Secondary plastid formed

KEY FEATURES

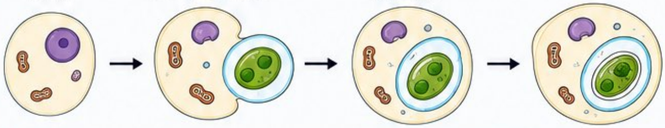
- Plastid has 3 or 4 membranes.
- The extra membranes are derived from the engulfed alga (plasma membrane) and the host vesicles.
- The algal nucleus is lost; genes transferred to host nucleus.
- Nucleomorph (remnant of algal nucleus) may be present.

EXAMPLES

- Euglenoids (e.g., *Euglena*)
- Dinoflagellates (e.g., *Peridinium*)
- Diatoms (e.g., Pinnularia)
- Brown algae (e.g., *Fucus*, Laminaria)
- Cryptophytes (e.g., *Cryptomonas*)

2. TERTIARY ENDOSYMBIOSIS

A eukaryote engulfs another eukaryote that already contains a secondary plastid.



① Heterotrophic eukaryote (host) → ② Engulfment of secondary-plastid bearing eukaryote → ③ Retention of endosymbiotic eukaryote → ④ Tertiary plastid formed

KEY FEATURES

- Plastid has 4 or more membranes.
- More complex origin than secondary plastid.
- Nucleomorph usually present.
- Additional membrane derived from the engulfed eukaryote.

EXAMPLES

- Dinoflagellates (e.g., *Noctiluca, Karenia*)
- Some ciliates with algal symbionts

3. COMPARISON OF PRIMARY, SECONDARY & TERTIARY ENDOSYMBIOSIS

Feature	Primary Endosymbiosis	Secondary Endosymbiosis	Tertiary Endosymbiosis
Host cell	Primitive eukaryote	Eukaryote (usually protist)	Eukaryote (protist)
Engulfed cell	Cyanobacterium	Photosynthetic alga	Eukaryote with secondary plastid
Result	Primary plastid	Secondary plastid	Tertiary plastid
No. of membranes around plastid	2	3 or 4	4 or more
Nucleomorph	Absent	Present in many	Usually present
Examples	Red algae, Green algae, Glaucophytes	Euglena, Dinoflagellates, Diatoms, Brown algae, Cryptophytes	Dinoflagellates (*Noctiluca*), certain ciliates
Significance	Origin of plastids	Great diversity of algae & protists	Further diversification & complexity

6. QUICK REVISION

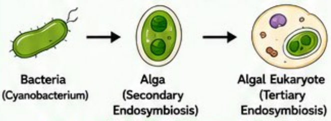
- **Primary:** Eukaryote engulfs cyanobacterium → 2 membranes.
- **Secondary:** Eukaryote engulfs alga → 3 or 4 membranes.
- **Tertiary:** Eukaryote engulfs eukaryote (with secondary plastid) → 4 or more membranes.
- More membranes = more complex endosymbiosis.
- Nucleomorph = algal nucleus remnant.

7. FREQUENTLY ASKED IGNOU EXAM POINTS

- Define secondary and tertiary endosymbiosis.
- Draw and label diagram of secondary and tertiary endosymbiosis.
- List organisms having secondary plastids.
- What is nucleomorph?
- How do secondary and tertiary plastids differ from primary plastids?
- Explain the significance of endosymbiosis.

8. MEMORY TRICK

"Bacteria → Alga → Algal Eukaryote"


Bacteria (Cyanobacterium)
Alga (Secondary Endosymbiosis)
Algal Eukaryote (Tertiary Endosymbiosis)

More partners, more membranes!

IN SHORT: Secondary endosymbiosis = Eukaryote eats Alga | Tertiary endosymbiosis = Eukaryote eats algal Eukaryote

MOLECULAR DRIVE vs MOLECULAR DIVERGENCE

Two opposite evolutionary forces acting at the molecular level

MOLECULAR DRIVE (Conservative Evolution)

- Refers to evolutionary changes that conserve the existing molecular structure and function.
- Acts to maintain similarity and stability.
- Operates through stabilizing selection and functional constraints.
- Results in molecular conservation (homology).

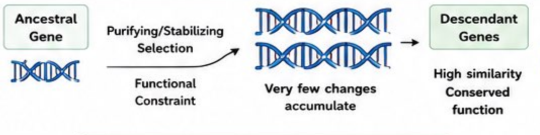
MOLECULAR DIVERGENCE (Progressive Evolution)

- Refers to evolutionary changes that lead to differences in molecular structure and function.
- Acts to generate diversity and novelty.
- Operates through mutation, natural selection, genetic drift and relaxed constraints.
- Results in molecular divergence (heterology).

MOLECULAR DIFFERENCES BETWEEN MOLECULAR DRIVE AND MOLECULAR DIVERGENCE

Feature	Molecular Drive	Molecular Divergence
Definition	Evolutionary process that preserves the existing molecular structure and function.	Evolutionary process that produces differences in molecular structure and function.
Molecular Level Change	Minimal or no change in nucleotide/amino acid sequences.	Accumulation of changes in nucleotide/amino acid sequences.
Type of Selection	Stabilizing selection; purifying selection.	Diversifying selection; directional selection; relaxed selection.
Genetic Mechanism	Functional constraints, stabilizing selection, gene conversion, purifying selection.	Mutation, genetic drift, recombination, gene duplication, relaxed constraints, positive selection.
Effect on Homology	Increases homology (similarity).	Decreases homology; increases heterology (differences).
Rate of Change	Slow rate of molecular change.	Relatively faster rate of molecular change.
Functional Outcome	Maintains existing function; conserves essential proteins and genes.	Produces new functions or modifies existing ones.
Examples	Conserved proteins: Cytochrome c, Histones, rRNA. Conserved genes for essential functions (e.g., glycolysis enzymes).	Divergent hemoglobin chains (α, β, γ), Immunoglobulins, Opsins, MHC genes.
Evolutionary Role	Maintains stability of vital molecules across species and over long periods.	Generates molecular diversity; raw material for evolution and adaptation.
Typical Outcome	Conservation → Similarity → Functional stability.	Divergence → Dissimilarity → Functional innovation.
Occurs Mainly In	Essential, housekeeping genes and molecules.	Non-essential or less constrained genes and molecules.
Molecular Signature	Low substitution rate; high sequence similarity; high purifying selection ($dN/dS < 1$).	Higher substitution rate; low sequence similarity; positive selection or relaxed constraint ($dN/dS \geq 1$).

MOLECULAR DRIVE – CONSERVATION



Ancestral Gene

Purifying/Stabilizing Selection

Functional Constraint

Very few changes accumulate

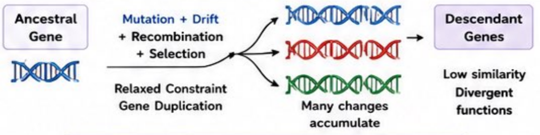
Descendant Genes

High similarity Conserved function

Leads to molecular similarity and conservation

VS

MOLECULAR DIVERGENCE – DIVERSIFICATION



Ancestral Gene

Mutation + Drift + Recombination + Selection

Relaxed Constraint Gene Duplication

Many changes accumulate

Descendant Genes

Low similarity Divergent functions

Leads to molecular dissimilarity and diversification

KEY POINTS

- ✓ Molecular drive preserves what works; molecular divergence explores what's new.
- ✓ Both processes operate together in evolution.
- ✓ Drive ensures survival of essential functions; divergence drives adaptation.
- ✓ Conservation and divergence are two sides of the same evolutionary coin.

EXAM TIP (IGNOU MZO-04)

For 5-mark answers, write definitions, mechanisms, effects, examples and significance of both molecular drive and divergence in a comparative manner using a table/flow diagram.

IN SHORT

Drive = Stability & Conservation

Divergence = Change & Diversification

Together they shape the molecular basis of evolution.

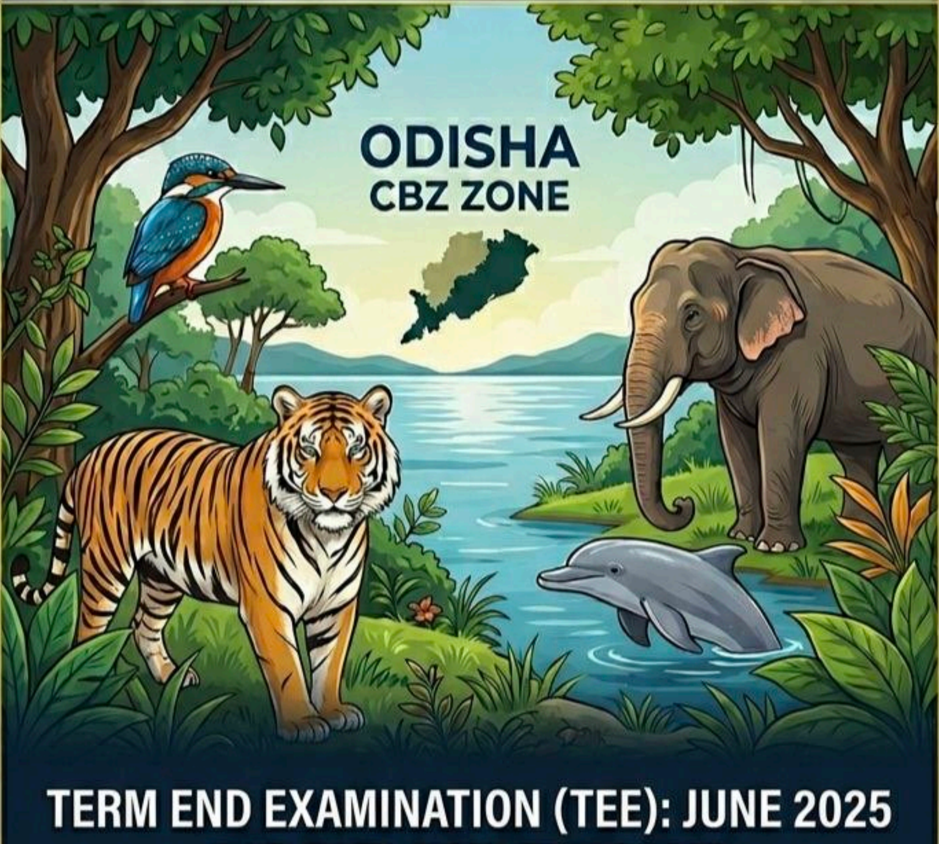
INDIRA GANDHI NATIONAL OPEN UNIVERSITY
IGNOU, MAIDAN GARHI, NEW DELHI - 110068

IGNOU MSc ZOOLOGY

PREVIOUS YEAR QUESTIONS (PYQs)

JUNE 2025 TERM END EXAMINATION

WITH ODISHA CBZ ZONE



TERM END EXAMINATION (TEE): JUNE 2025
SUBJECT: ZOOLOGY (MSC)

No. of Printed Pages : 3 **MZO–004**

M. SC. (ZOOLOGY)

(MSCZOO)

Term-End Examination

June, 2025

MZO-004 : SYSTEMATICS, BIODIVERSITY AND EVOLUTION

Time : 2 Hours *Maximum Marks : 50*

Note : *Attempt any* ***five*** *questions. All questions carry equal marks.*

1. (a) Explain the propositions given in the Darwinian theory of evolution. 6

   (b) Write the applications of molecular clock. 4

2. (a) Explain the Urey Miller experiment with the help of a well labelled diagram. 6

   (b) Describe the hypothesis proposed for the origin of genetic code. 4

3. (a) Discuss the methods of inferring the evolutionary data. 5

   (b) Describe the different softwares used for phylogenetic tree reconstruction. 5

4. (a) How alternative splicing and exon shuffling have contributed to the evolution of eukaryotic genome ? 5

   (b) Classify the bacteria and archaea into various groups based on their preferred habitats giving suitable examples of each. 5

5. Describe the origin of mitochondria and chloroplasts through endosymbiosis with suitable examples. 10

6. (a) Discuss in detail the five-kingdom systems of classification. 5

   (b) Write brief notes on sympatric and parapetric speciation. 5

7. Describe the following : 5+5

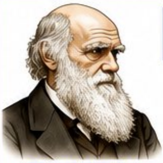
   (a) Genomic islands

   (b) History of evolution of *Homo sapiens*

× × × × ×

DARWINIAN THEORY OF EVOLUTION

Propositions of Darwinism



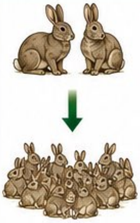
Charles Darwin
(1809–1882)

Darwinian theory of evolution by natural selection explains how species have changed over time from common ancestors through a natural process.

Darwin developed his theory based on observations, especially from Galápagos Islands (1831–36).

PROPOSITIONS OF DARWINIAN THEORY

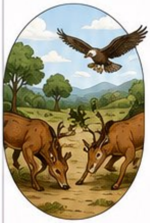
1. OVERPRODUCTION



- Organisms produce large number of offspring.
- More offspring are produced than can possibly survive.
- This leads to a struggle for existence.

Example: A pair of rabbits can produce thousands of offspring in a few years.

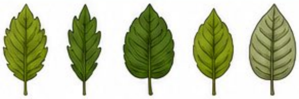
2. STRUGGLE FOR EXISTENCE



- Because of overproduction, resources such as food, space, mates are limited.
- Organisms must compete with each other and with environmental conditions.
- Struggle is universal – occurs among individuals of same species, different species and with nature.

Example: In a herd of deer, individuals compete for food and mates.

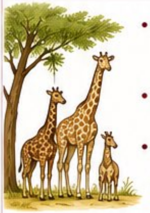
3. VARIATION



- Individuals in a population show variations in their characteristics.
- Variations may be in size, colour, shape, behaviour, etc.
- Some variations are inherited while others are acquired (non-inheritable).

Example: Leaves of a plant vary in size and shape.

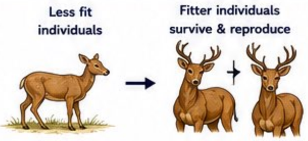
4. SURVIVAL OF THE FITTEST



- Among the variations, some individuals are better suited (fitter) to the environment.
- Fitter individuals have higher chances of survival.
- "Survival of the fittest" means survival of those that are best adapted.

Example: Giraffes with longer necks could reach food better and survived more.

5. NATURAL SELECTION

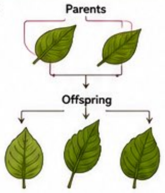


- Nature (environment) selects the fittest.
- Less fit individuals are eliminated.
- Fitter individuals survive, reproduce and pass on their favourable traits.

Example: Stronger and healthier deer survive harsh winter and reproduce.

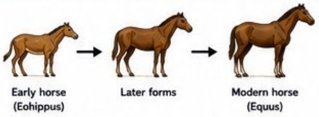
6. INHERITANCE OF FAVOURABLE VARIATIONS

- Favourable variations are inherited by offspring.
- These variations accumulate over generations.
- Leads to gradual evolution.



Example: Offspring inherit long neck trait and the population shows more long-necked giraffes.

7. DESCENT WITH MODIFICATION



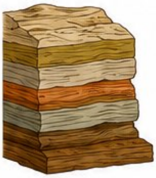
- Over long periods, accumulation of favourable variations leads to changes in populations.
- New species arise from pre-existing species.
- All species are related through "descent with modification" from common ancestors.

Example: Evolution of horse from small, many-toed ancestor to large, single-toed modern horse.

THE PROCESS OF EVOLUTION (Darwinism)

Overproduction
↓
Struggle for existence
↓
Variation
↓
Survival of the fittest
↓
Natural selection
↓
Inheritance of favourable variations
↓
Descent with modification
↓
EVOLUTION

8. GRADUALISM



- Evolution is slow and gradual.
- It occurs over millions of years.
- Changes are small but continuous.

Example: Formation of sedimentary rocks layer by layer over long periods.

KEY POINTS TO REMEMBER

- ✓ Darwinism is based on observations and evidence.
- ✓ Environment selects; it does not create changes.
- ✓ Fittest means "best suited" not "strongest".
- ✓ Evolution is a natural, continuous and gradual process.
- ✓ All living beings are related through common ancestry.

SIGNIFICANCE OF DARWINIAN THEORY

- ★ Provided scientific explanation for evolution.
- ★ Unified all biological sciences.
- ★ Basis for modern evolutionary biology.
- ★ Explains adaptation, diversity and extinction.
- ★ Supports the concept of common descent.

CRITICISMS (Later Addressed)

- Did not explain source of variations (later by Genetics).
- Did not explain mechanism of inheritance (Mendel's work).
- Later integrated with genetics – Modern Synthesis.

IN SHORT

Darwin proposed that species evolve by natural selection. Overproduction leads to struggle, variation gives some individuals an advantage, nature selects the fittest, and favourable traits are inherited. Over time, new species arise.

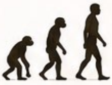
FREQUENTLY ASKED IN EXAMS

① State the propositions of Darwinism.
② Explain natural selection.
③ Discuss struggle for existence.
④ What is meant by "survival of the fittest"?
⑤ Explain descent with modification with example.

MEMORY TRICK

"O S V S N I D G"

O – Overproduction
S – Struggle
V – Variation
S – Survival of the fittest
N – Natural selection
I – Inheritance
D – Descent with modification
G – Gradualism



APPLICATIONS OF MOLECULAR CLOCK

The molecular clock hypothesis states that genetic mutations accumulate at a relatively constant rate over time. By comparing DNA or protein sequences, we can estimate the time of evolutionary events. This concept has wide applications in biological research.

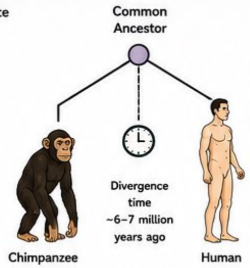
MAJOR APPLICATIONS

1. ESTIMATION OF DIVERGENCE TIME

Molecular clock helps to estimate the time when two species or genes diverged from a common ancestor.

Used to construct a timeline of evolutionary events.

Example:
Human-Chimpanzee divergence estimated at ~6–7 million years ago.

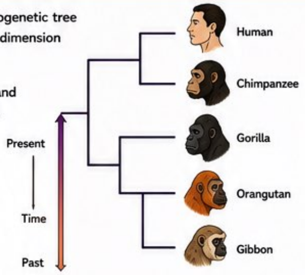

Common Ancestor
Divergence time ~6–7 million years ago
Chimpanzee
Human

2. CONSTRUCTION OF MOLECULAR PHYLOGENIES

Provides a time-calibrated phylogenetic tree (chronogram) by adding a time dimension to evolutionary relationships.

Helps to understand the order and timing of lineage diversification.

Example:
Evolutionary relationships among primates, rodents or flowering plants.

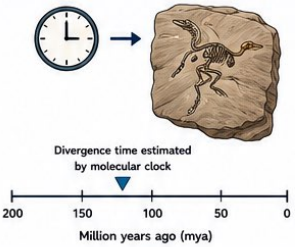

Human
Chimpanzee
Gorilla
Orangutan
Gibbon
Present
Time
Past

3. CALIBRATION OF THE FOSSIL RECORD

Molecular clock provides independent estimates of divergence times that can be compared with fossil dates.

Helps in dating fossils and filling gaps in the fossil record.

Example:
Dating of early mammals or birds using DNA sequence data to supplement scarce fossils.


Divergence time estimated by molecular clock
200
150
100
50
0
Million years ago (mya)

4. STUDY OF RATE OF EVOLUTION

Helps to compare evolutionary rates among different genes, lineages or taxa.

Identifies fast-evolving and slow-evolving genes.

Example:
Mitochondrial genes evolve faster than nuclear genes; used in population and phylogeographic studies.

Gene	Relative Rate of Evolution
Mitochondrial cytochrome b	Fast
rRNA genes	Slow
Histone genes	Very slow
Morphological traits	Variable

Fast

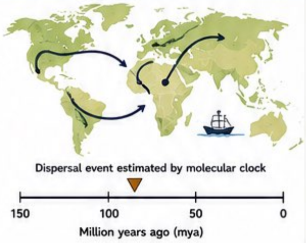
↓

Slow

5. BIOGEOGRAPHY AND DISPERSAL EVENTS

Molecular clock helps to estimate the timing of colonization, migration and dispersal events across geographic areas.

Example:
Peopling of continents, spread of pathogens, or dispersal of island species.

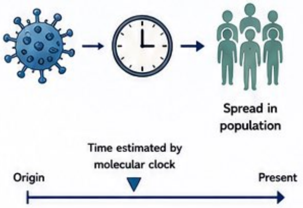

Dispersal event estimated by molecular clock
150
100
50
0
Million years ago (mya)

6. EPIDEMIOLOGY AND PUBLIC HEALTH

Used to estimate the time of emergence and spread of pathogens (viruses, bacteria).

Helps in tracking outbreaks and understanding the evolution of drug resistance.

Example:
Dating the origin of HIV-1, influenza strains or antibiotic-resistant bacteria.

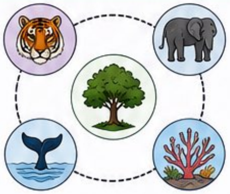

Spread in population
Time estimated by molecular clock
Origin
Present

7. CONSERVATION BIOLOGY

Helps to identify evolutionarily significant units (ESUs) and management units.

Guides conservation priorities by understanding evolutionary history and distinct lineages.

Example:
Identifying distinct lineages of tigers, whales or corals for conservation planning.

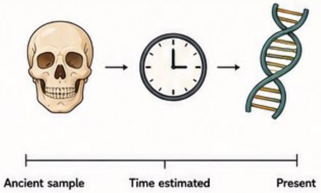


8. FORENSICS AND ANTHROPOLOGY

Helps to estimate the age of samples and the timing of human evolutionary events.

Useful in resolving forensic cases and studying ancient DNA.

Example:
Dating ancient human remains or identifying maternal lineages.


Ancient sample
Time estimated
Present

KEY POINTS

- Based on the constant rate of molecular evolution.
- Uses DNA or protein sequence differences.
- Provides estimates of time for evolutionary events.
- Complements fossil record and other methods.

SIGNIFICANCE

- ✓ Bridges molecular data with evolutionary time.
- ✓ Essential tool in evolutionary biology, systematics, epidemiology and conservation.
- ✓ Helps reconstruct the history of life on Earth.

IN SHORT: Molecular clock converts genetic differences into time, enabling us to understand when life's major events happened and how species evolved and spread across the Earth.

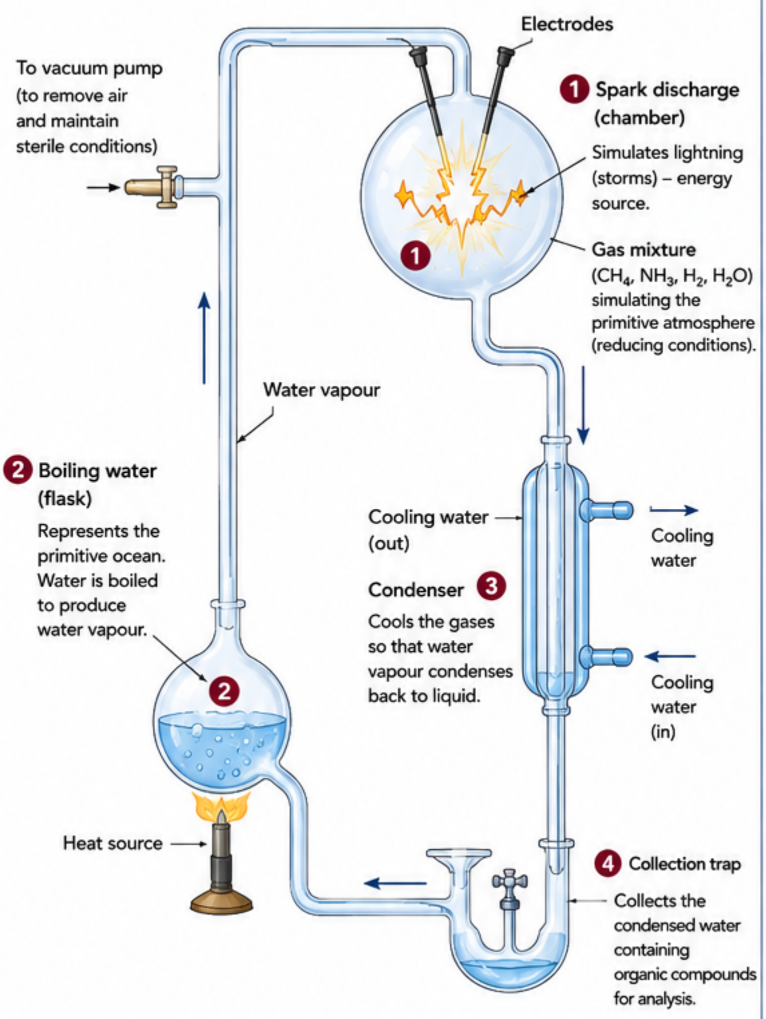
(a)

The Urey–Miller Experiment

(A Simulation of Early Earth Conditions)

The Urey–Miller experiment (1953) tested the hypothesis that organic molecules could have formed abiotically on the primitive Earth.

WELL LABELLED DIAGRAM OF THE APPARATUS


Electrodes
To vacuum pump (to remove air and maintain sterile conditions)
① Spark discharge (chamber)
Simulates lightning (storms) – energy source.
①
Gas mixture (CH_4, NH_3, H_2, H_2O) simulating the primitive atmosphere (reducing conditions).
Water vapour
② Boiling water (flask)
Represents the primitive ocean. Water is boiled to produce water vapour.
②
Cooling water (out)
Condenser ③
Cools the gases so that water vapour condenses back to liquid.
Cooling water
Cooling water (in)
Heat source
④ Collection trap
Collects the condensed water containing organic compounds for analysis.

The entire apparatus is a closed system. The gases circulate continuously through the system during the experiment.

EXPERIMENT: STEPS

1. A mixture of gases (methane–CH_4, ammonia–NH_3, hydrogen–H_2 and water vapour–H_2O) thought to be present in the primitive Earth's atmosphere was introduced into the apparatus.
2. Water in the flask was boiled to generate water vapour.
3. The vapour mixed with the gases and passed into the spark discharge chamber, where electric sparks (simulating lightning) were passed for about a week (7 days).
4. The gases were then cooled in the condenser, and the water (now containing products) collected in the trap.
5. The solution was analysed for organic compounds.

CONDITIONS SIMULATED

- Reducing atmosphere (no free oxygen)
- Energy source – lightning (electric sparks)
- Primitive ocean (boiling water)
- Long duration to allow chemical reactions

RESULTS

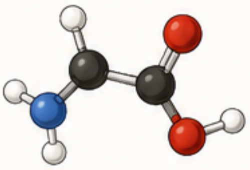
The collected sample contained a variety of organic compounds, including:

- Amino acids (e.g., glycine, alanine, aspartic acid)
- Urea
- Organic acids
- Sugars
- Other carbon compounds

This showed that simple organic molecules can be formed spontaneously from inorganic substances under conditions thought to exist on early Earth.

SIGNIFICANCE

- ✓ Provided the first experimental evidence supporting chemical evolution—organic molecules can form abiotically from inorganic precursors.
- ✓ Amino acids, the building blocks of proteins, can form without life.
- ✓ Supported the Oparin–Haldane hypothesis about the origin of life.
- ✓ Helped explain how the raw materials for life could have accumulated in the primitive oceans, leading to the origin of life.



(Example: Glycine)

CONCLUSION

The Urey–Miller experiment demonstrated that under primitive Earth conditions, organic molecules could be synthesized abiotically. These molecules could have accumulated in the oceans and, over time, led to more complex polymers and the origin of life.

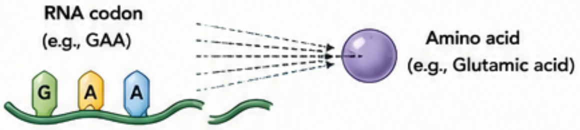
(b) Hypotheses for the Origin of the Genetic Code

The genetic code is the set of rules by which nucleotide triplets (codons) specify amino acids or stop signals during protein synthesis.

Several hypotheses propose how the code arose from prebiotic chemistry and early molecular evolution to become the nearly universal, unambiguous system seen in all living organisms today.

1. STEREOCHEMICAL HYPOTHESIS (Crick)

The code originated from direct chemical interactions between codons and amino acids based on their stereochemical properties.



Codons and amino acids with complementary shapes and charge properties bound specifically.

Limitations: Cannot explain all assignments; many codon–amino acid pairs lack obvious stereochemical affinity.

2. CO-EVOLUTION (OR ADAPTATION) HYPOTHESIS

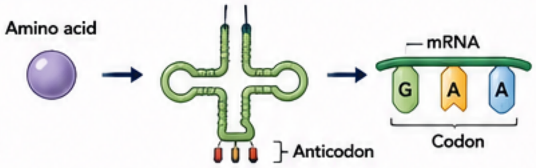
The code evolved gradually through mutual adaptation between codons and amino acids (and later, tRNAs and proteins).

Early stage Random assignments of amino acids to codons → Peptides with some functions were selected → tRNAs and translation machinery evolved → Code became optimized, stable and universal

Supported by: universality of the code and its error-minimizing properties (similar codons code for similar amino acids).

3. ADAPTOR (tRNA) HYPOTHESIS (Crick)

tRNAs were the first molecules to adapt amino acids, and codons were later assigned to these aminoacyl-tRNAs.



Early tRNAs recognized amino acids.
Codons evolved to pair with tRNA anticodons.

Supported by: central role of tRNA in modern translation and conservation of tRNA structure.

4. ERROR MINIMIZATION HYPOTHESIS (Di Giulio)

The code evolved to minimize the harmful effects of translation errors. It is "optimized" so that single-base changes often result in substitution of similar amino acids.

Wobble & Degeneracy

Codons

GUU
GUC
GUA
GUG

All code for Valine (Val)

Minimization

Single-base change (error)

GAA (Glu) → Same amino acid (less harmful)

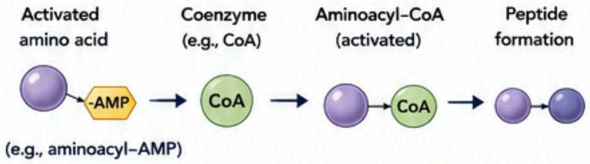
GAG (Glu)

AAA (Lys) → Different amino acid (more harmful)

Supported by: quantitative analyses show the code is better than random in minimizing the impact of errors.

5. METABOLIC-COENZYME HYPOTHESIS (Wong)

Amino acids were first incorporated into peptides in the context of metabolic pathways using activated intermediates (coenzymes). The genetic code was recruited later.



Supported by: existence of aminoacyl-tRNA synthetases and metabolic roles of amino acids in early life.

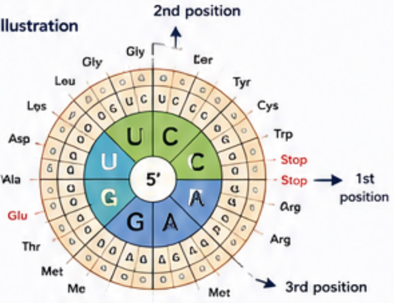
6. BIOSYNTHETIC / CHEMICAL AFFINITY HYPOTHESIS

Assignments reflect chemical affinities, biosynthetic relationships or shared functional properties.

Examples of patterns

- Hydrophobic amino acids ↔ codons with U/C
- Polar amino acids ↔ A-rich codons
- Biosynthetic families often coded by related codons (e.g., Asp (GAU, GAC) and Asn (AAU, AAC))

Illustration

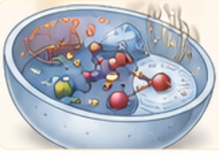


Suggests the code is not random but influenced by chemistry and early metabolic networks.

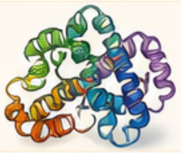
COMMON FEATURES OF ALL HYPOTHESES

- The code arose gradually in stages.
- An RNA world likely preceded the code.
- Co-adaptation between RNAs, amino acids and proteins was crucial.
- Natural selection refined the code to its present form.
- Universality and error tolerance are hallmarks of an optimized system.

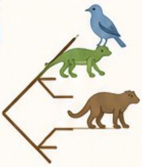
IN SUMMARY



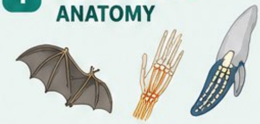
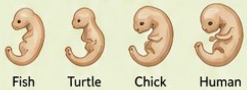
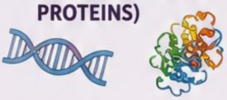
The origin of the genetic code was a gradual evolutionary process driven by chemical affinities, molecular co-evolution, selection for functional efficiency and error minimization, ultimately producing the nearly universal code that links nucleic acids to proteins.



METHODS FOR INFERRING EVOLUTIONARY DATA



Evolutionary data come from many sources. Different methods provide complementary lines of evidence to reconstruct the history of life.

METHOD	WHAT IT USES / MEASURES	WHAT IT INFORMS	EXAMPLES
1 COMPARATIVE ANATOMY 	Structures of organisms (bones, muscles, organs) and their similarities and differences.	• Homologous structures indicate common ancestry. • Analogous structures suggest convergent evolution.	Forelimbs of human, bat, and whale show homology, indicating shared ancestry among mammals.
2 COMPARATIVE EMBRYOLOGY 	Early developmental stages of embryos across species.	• Similar early development suggests common ancestry. • Differences reveal divergent evolution.	Vertebrate embryos share features (e.g., pharyngeal pouches, tails) early in development.
3 FOSSIL RECORD 	Preserved remains, impressions, and traces in rock layers (strata) through geological time.	• Reveals past diversity and extinction. • Shows transitional forms. • Helps date lineages and events.	Fossils of transitional whales show evolution from land mammals to aquatic forms.
4 MOLECULAR DATA (DNA / RNA / PROTEINS) 	Nucleotide or amino acid sequences and their similarities and differences.	• Detects genetic relatedness. • Estimates divergence times (molecular clock). • Resolves evolutionary relationships.	DNA comparisons show humans and chimpanzees are ~98–99% similar, indicating close common ancestry.
5 BIOGEOGRAPHY 	Geographic distribution patterns of species and lineages.	• Explains how species distributions arose. • Indicates historical connections (e.g., continental drift, dispersal, vicariance).	Marsupials are diverse in Australia but rare elsewhere, consistent with long isolation of that region.
6 ECOLOGICAL & BEHAVIORAL DATA 	Traits, interactions, niches, and behaviors of organisms.	• Reveals adaptive evolution and natural selection. • Explains trait evolution in context.	Beak shapes of finches relate to diets; bower building reflects sexual selection and species diversification.
7 PHYLOGENETIC ANALYSIS 	Integrated analysis of multiple data types using statistical and computational methods to build evolutionary trees.	• Produces tested hypotheses of relationships. • Allows estimation of ancestral traits and evolutionary history.	A phylogenetic tree summarizes relationships among species based on combined evidence from many data sources.

MULTIPLE LINES OF EVIDENCE

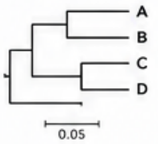
No single method tells the whole story. Using independent methods together provides a more robust and reliable picture of evolution.

3 (b) SOFTWARES USED FOR PHYLOGENETIC TREE RECONSTRUCTION

Phylogenetic software packages use different algorithms and models to infer evolutionary relationships from molecular or morphological data and display trees.

1. MEGA (Molecular Evolutionary Genetics Analysis)

MEGA



A widely used, user-friendly tool for sequence analysis and phylogenetic tree reconstruction.

Key Features

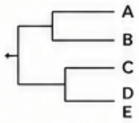
- Sequence alignment (built-in ClustalW, MUSCLE)
- Model selection and evolutionary distance analysis
- Tree building: NJ, UPGMA, Maximum Parsimony (MP), Maximum Likelihood (ML)
- Bootstrap support and tree visualization
- Molecular clock and demographic analyses

Best for: Beginners and intermediate users; teaching and publication-quality trees.

Platform: Windows, macOS, Linux

2. PAUP* (Phylogenetic Analysis Using Parsimony)

PAUP✳



One of the earliest and most powerful tools for phylogenetic analysis, especially parsimony.

Key Features

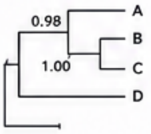
- Heuristic and exhaustive Maximum Parsimony
- Distance methods (NJ, UPGMA)
- Likelihood (with external programs) and character weighting
- Bootstrapping, jackknifing, Bremer support
- Handles large and complex datasets

Best for: Parsimony analyses; advanced users.

Platform: Windows, macOS (paid)

3. MrBayes

MrBayes



Bayesian inference software widely used for phylogenetic estimation.

Key Features

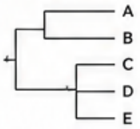
- Bayesian inference using MCMC sampling
- Supports nucleotide, amino acid and morphological data
- Model selection (with mixed models)
- Posterior probabilities for clades
- Can be run via command line or GUI (e.g., MrBayesGUI)

Best for: Bayesian phylogenetic inference; robust statistical framework.

Platform: Cross-platform (command line); Windows (GUI), macOS, Linux

4. RAxML / RAxML-NG

RAxML



Optimized for Maximum Likelihood analysis of large molecular datasets.

Key Features

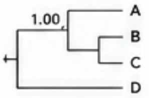
- Fast ML tree inference for large alignments
- Many substitution models
- Bootstrap (rapid bootstrap) and ML search
- RAxML-NG: faster, parallelized, memory efficient
- Handles partitioned datasets

Best for: Large-scale ML analyses; high performance computing.

Platform: Linux, Unix, macOS, Windows (via WSL)

5. IQ-TREE

IQ-TREE



Fast and effective Maximum Likelihood phylogenetic inference.

Key Features

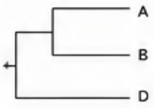
- Automatic model selection (ModelFinder)
- Ultrafast bootstrap approximation (UFBoot)
- SH-aLRT branch support
- Handles partitioned data, site-heterogeneous models
- Very fast and accurate

Best for: Fast, accurate ML treee:.fl trees; large datasets; most widely used today.

Platform: Cross-platform (Windows, macOS, Linux)

6. PhyML

PhyML



Maximum Likelihood phylogenetic inference using analytical approximations.

Key Features

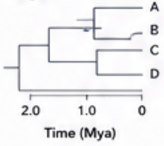
- Fast ML tree reconstruction
- Many substitution models
- Bootstrap support
- Handles large alignments with speed and accuracy
- User-friendly interface (PhyML 3 web server / GUI)

Best for: ML analysis with good balance of speed and accuracy.

Platform: Cross-platform; Web server and standalone versions

7. BEAST / BEAST 2

beast



Bayesian software for phylogenetics with temporal and evolutionary analyses.

Key Features

- Bayesian inference with time calibration (molecular clock)
- Coalescent-based species tree estimation
- Ancestral state reconstruction, phylogeography
- Model selection and complex substitution models
- BEAUti for GUI, Tracer for analysis

Best for: Phylogenetics with divergence time estimation and coalescent analyses.

Platform: Cross-platform (requires Java)

8. PhyloSuite

PhyloSuite

An integrated platform for molecular phylogenetics and evolution.

Key Features

- Multiple alignment, model selection, tree building (ML, BI, MP)
- Data partitioning and concatenation
- Supports IQ-TREE, RAxML, MrBayes, PhyML, etc.
- Visualization and tree annotation
- Easy-to-use, all-in-one platform

Best for: All-in-one solution for phylogenetic workflow.

Platform: Windows, macOS, Linux

COMPARISON AT A GLANCE

Software	Main Method(s)	Best For	Ease of Use	Speed	Dataset Size
MEGA	NJ, UPGMA, MP, ML	Beginners, teaching	High	Moderate	Small–Medium
PAUP*	Parsimony, Distance	Parsimony, complex character analysis	Medium	Moderate	Small–Large
MrBayes	Bayesian Inference	Bayesian trees	Medium	Slow–Moderate	Small–Large
RAxML / NG	Maximum Likelihood	Large datasets (ML)	Medium (CLI)	Very Fast	Large–Very Large
IQ-TREE	Maximum Likelihood	Fast & accurate ML	High (CLI)	Very Fast	Large–Very Large
PhyML	Maximum Likelihood	ML with good speed	High	Fast	Medium–Large
BEAST 2	Bayesian (Time trees)	Divergence time, coalescent	Medium (GUI)	Slow	Small–Large
PhyloSuite	Multiple (integrated)	Integrated workflow	High	Depends on tool	Small–Very Large

GENERAL WORKFLOW (COMMON TO MOST TOOLS)

① Collect sequences / morphological data

② Multiple sequence alignment

③ Model selection / Data partitioning (if needed)

④ Tree reconstruction (choose method)

⑤ Assess support (Bootstrap / Posterior / SH-aLRT)

⑥ Visualize, annotate and interpret the tree

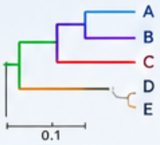
TIPS FOR CHOOSING SOFTWARE

- ☑ For beginners and teaching: MEGA, PhyloSuite
- ☑ For parsimony: PAUP*
- ☑ For Bayesian analysis: MrBayes, BEAST 2
- ☑ For large ML datasets: IQ-TREE, RAxML-NG
- ☑ For time-calibrated trees: BEAST 2

No single program is best for all situations. Choice depends on data type, research question, method required, dataset size and user expertise.

OUTPUT

- Phylogenetic tree (rooted or unrooted)
- Branch support values
- Estimates of divergence times (if applicable)
- Evolutionary interpretations



(a)

How Alternative Splicing and Exon Shuffling Have Contributed to the Evolution of Eukaryotic Genome?

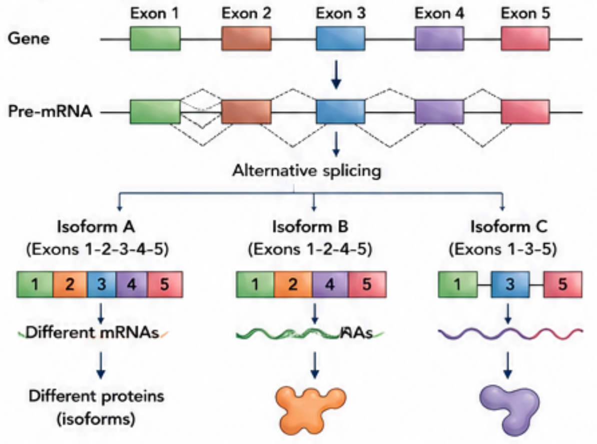
Eukaryotic genomes are complex and highly dynamic. Two major mechanisms—alternative splicing and exon shuffling—have greatly increased proteomic diversity and facilitated the evolution of new genes and functions.

1. ALTERNATIVE SPLICING (AS)

What is it?

A process in which different combinations of exons are joined together after transcription from the same pre-mRNA, producing multiple mature mRNA transcripts and protein isoforms.

How it works



Types of alternative splicing

- Exon skipping (cassette exon)
- Mutually exclusive exons
- Alternative 5′ splice site
- Alternative 3′ splice site
- Intron retention

Key features

- Occurs post-transcriptionally
- Regulated by splicing factors (SR proteins, hnRNPs)
- Tissue/development/stimulus-specific

Contributions to Evolution

- ✓ Increases proteomic diversity without increasing gene number.
- ✓ Allows rapid functional innovation and fine-tuning of gene function.
- ✓ Provides raw material for evolution of new functions.
- ✓ Facilitates adaptation to different developmental stages and environments.
- ✓ Mis-splicing or novel splicing patterns can lead to new gene functions.

Examples

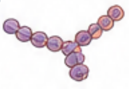
Drosophila Dscam1 gene

- > 38,000 isoforms generated by alternative splicing.
- Crucial for neural wiring and immune recognition.

Vertebrate tropomyosin gene

- Different isoforms in muscle, brain, and other tissues.
- Tissue-specific functions.

Human calcitonin / CGRP gene



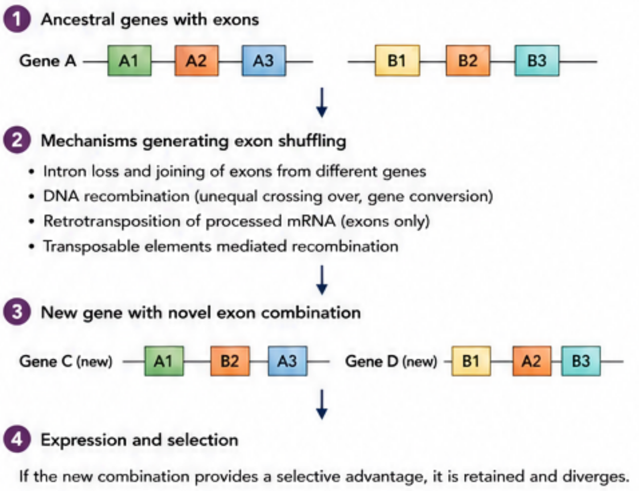
- Alternative splicing produces calcitonin (thyroid) and CGRP (neurons).
- Different physiological roles.

2. EXON SHUFFLING (EXON RECOMBINATION)

What is it?

A process in which exons (coding sequences) are recombined during evolution to form new genes or new exon combinations within existing genes.

How it works



① Ancestral genes with exons

② Mechanisms generating exon shuffling

- Intron loss and joining of exons from different genes
- DNA recombination (unequal crossing over, gene conversion)
- Retrotransposition of processed mRNA (exons only)
- Transposable elements mediated recombination

③ New gene with novel exon combination

④ Expression and selection

If the new combination provides a selective advantage, it is retained and diverges.

Contributions to Evolution

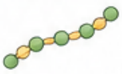
- ✓ Creates entirely new genes and domain architectures.
- ✓ Generates proteins with new functions and interactions.
- ✓ Major driver of domain evolution and modularity.
- ✓ Speeds up evolution by reusing existing functional modules.
- ✓ Responsible for emergence of multi-domain proteins and new protein families.

Examples

Immunoglobulin (Ig) genes

- Exons encoding variable (V), diversity (D), and joining (J) regions recombined.
- Generated vast diversity in antigen-binding proteins.

Fibronectin gene



- Composed of repeated domains (type I, II, III).
- Thought to have evolved by exon shuffling and duplication of ancestral exons.

Protein kinase genes

- Many kinases share conserved catalytic domains but different regulatory domains.
- Arise through exon shuffling and duplication.

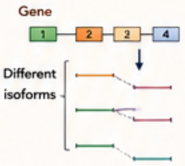
COMBINED IMPACT ON EUKARYOTIC GENOME EVOLUTION

- Greatly increases proteome complexity compared to prokaryotes.
- Enables functional innovation and neofunctionalization.
- Provides flexibility to respond to developmental and environmental changes.
- Contributes to gene family expansion and evolution of complex biological systems.
- Major role in the emergence of multi-domain proteins and new signaling/ regulatory networks.

KEY TAKEAWAYS

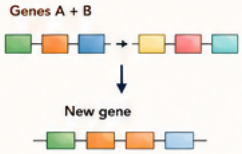
Alternative Splicing

- ✓ Generates multiple isoforms from a single gene.
- ✓ Increases proteomic and functional diversity.
- ✓ Facilitates adaptation and tissue-specific functions.



Exon Shuffling

- ✓ Recombines exons to create new genes.
- ✓ Generates novel domain architectures.
- ✓ Drives evolution of new functions and protein families.



Together, alternative splicing and exon shuffling are powerful evolutionary mechanisms that have shaped the complexity, adaptability and diversity of eukaryotic life.

4 1. (b)

Classification of Bacteria and Archaea Based on Their Preferred Habitats

Bacteria and archaea occupy a wide range of habitats. Based on their preferred (optimal) environmental conditions, they can be classified into the following ecological (habitat-based) groups.

A. BACTERIA – Classified by Preferred Habitat

Group (Habitat)	Environmental Conditions	Key Features	Examples (Genera / Species)	Typical Habitat / Example
1. Psychrophiles (cold-loving)	Optimum: ≤ 15 °C Grows at 0–20 °C (pH 6–8) Often in marine or polar environments	• Enzymes adapted to low temperature • Membrane rich in unsaturated fatty acids • Grow slowly	• *Polaribacter* spp. • *Psychrobacter* spp. • *Colwellia psychrerythraea* • *Shewanella frigidimarina*	 Polar seas, deep oceans, ice, glacial habitats
2. Mesophiles (moderate-loving)	Optimum: 20–45 °C Grows at 15–45 °C (pH ~6.5–7.5) Most common bacteria	• Enzymes active at moderate temperature • Wide metabolic versatility • Include many pathogens and decomposers	• *Escherichia coli* • *Bacillus subtilis* • *Staphylococcus aureus* • *Lactobacillus* spp.	 Soil, water, animals, human body, food
3. Thermophiles (heat-loving)	Optimum: 45–80 °C Grows at 45–85 °C (pH ~5–8) Require high temperature	• Heat-stable enzymes • Membrane lipids more saturated • Many are spore formers	• *Bacillus stearothermophilus* • *Thermus aquaticus* • *Geobacillus* spp. • *Caldicellulosiruptor* spp.	 Hot springs, compost heaps, geothermal soils
4. Hyperthermophiles (extreme heat-loving)	Optimum: 80–110 °C Grows at 80–113 °C (pH ~5–7) Require very high temperature	• Extreme heat stability • Ether-linked lipids (in some) • Specialized chaperone proteins	• *Thermococcus kodakarensis* • *Pyrococcus furiosus* • *Aquifex aeolicus*	 Deep-sea hydrothermal vents, hot submarine vents
5. Acidophiles (acid-loving)	Optimum: pH ≤ 3 Many grow at pH 0–5 (Many are moderate thermophiles too)	• Acid-stable enzymes and cell envelope • Maintain low internal pH • Often chemolithotrophs	• *Acidithiobacillus ferrooxidans* • *Thiobacillus thiooxidans* • *Sulfolobus acidocaldarius* (archaeal example shown here for similarity)	 Acidic soils, acid mine drainage, hot springs
6. Alkaliphiles (alkali-loving)	Optimum: pH 8.5–11 Grows at pH 8–12 Often moderate thermophiles	• Alkalistable enzymes • Specific adaptations for membrane transport and DNA stability	• *Bacillus halodurans* • *Natronobacterium gregoryi* • *Spiribacter salinus*	 Soda lakes, alkaline soils, detergents, tanning effluents
7. Halophiles (salt-loving)	Optimum: ≥ 2–25% NaCl Some need very high salt (up to saturated brine ~30% NaCl)	• Require high salt for growth • "Salt-in" (cytoplasm) or "salt-out" (adaptation) strategies	• *Halobacterium salinarum* (archaea) • *Haloferax mediterranei* (archaea) • *Chromohalobacter salexigens* (bacterium)	 Salt lakes, salterns, saline soils, seawater

B. ARCHAEA – Classified by Preferred Habitat

Group (Habitat)	Environmental Conditions	Key Features	Examples (Genera / Species)	Typical Habitat / Example
1. Methanogens (anaerobic)	Anaerobic Optimum: 30–40 °C (pH ~6.5–7.5) Require reducing conditions	• Produce methane (CH_4) • Unique ether-linked lipids • Important in global carbon cycle	• *Methanobacterium formicicum* • *Methanococcus maripaludis* • *Methanosarcina barkeri*	 Swamps, rice fields, ruminant gut, sediments, landfills
2. Extreme Halophiles (salt-loving)	Optimum: 3–5 M NaCl (15–30% salt) pH ~6–8	• Require high salt for growth • Red-pigmented (bacteriorhodopsin) • Ether-linked lipids	• *Halobacterium salinarum* • *Haloferax volcanii* • *Halorubrum* spp.	 Salt lakes, salterns, salt pans, hypersaline environments
3. Thermoacidophiles (heat and acid loving)	Optimum: 60–80 °C pH 1–3	• Grow in hot, acidic environments • Unique cell structures, stable enzymes	• *Sulfolobus acidocaldarius* • *Thermoplasma acidophilum*	 Hot springs, volcanic areas, acid mine drainage
4. Hyperthermophiles	Optimum: 80–105 °C Some up to 113 °C pH ~5–8	• Extremely heat stable • Many are anaerobic • Ether-linked lipid membranes	• *Pyrococcus furiosus* • *Thermococcus kodakarensis* • *Archaeoglobus fulgidus*	 Deep-sea vents, hot submarine vents

Key Points

- Habitat strongly influences the physiology and biochemistry of microbes.
- Extremophiles show remarkable adaptations in enzymes, membranes and cell structures.
- These microbes play vital roles in nutrient cycling, biotechnology and ecosystem balance.

Types of Extremes

- Cold (Psychrophiles)
- Heat (Thermophiles / Hyperthermophiles)
- pH (Acidophiles / Alkaliphiles)
- Salt (Halophiles)
- Anaerobic Methane Production (Methanogens)

Significance

- Bioremediation, waste treatment
- Industrial enzymes (detergents, PCR, etc.)
- Bioenergy (biogas, hydrogen)
- Extreme environment exploration (space, deep sea, Mars analogs)
- Understanding the limits and adaptability of life

Bacteria and archaea exhibit extraordinary diversity by colonizing habitats from polar ice to boiling vents, from acidic pools to salty lakes, thereby driving evolution and sustaining life in diverse environments.

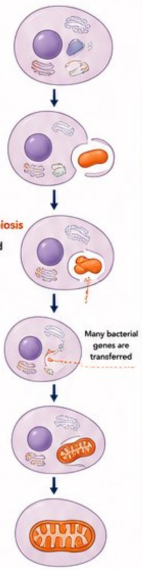
Origin of Mitochondria and Chloroplasts through Endosymbiosis

The endosymbiotic theory proposes that mitochondria and chloroplasts originated from free-living prokaryotes that were engulfed by an ancestral eukaryotic host cell and established a mutually beneficial (symbiotic) relationship.

- 🟧 Aerobic bacterium (α-proteobacterium)
- 🟩 Photosynthetic bacterium (cyanobacterium)
- ● Ancestral eukaryotic host (archaeal-like cell)

A. ORIGIN OF MITOCHONDRIA

Proposed event: ~1.6–2.0 billion years ago



① **Ancestral host cell**
An archaeal-like eukaryotic cell with nucleus and endomembrane system but no mitochondria.

② **Engulfment**
The host cell engulfs an aerobic α-proteobacterium.

③ **Establishment of endosymbiosis**
The bacterium is not digested and both partners benefit.

④ **Integration**
Gene transfer from the bacterium to the host nucleus begins.

⑤ **Coevolution**
The endosymbiont becomes essential; reduced genome and specialized functions.

⑥ **Modern mitochondrion**
The endosymbiont evolves into a mitochondrion.

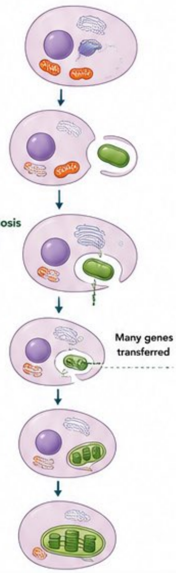
Evidence

- Double membrane (inner like bacteria, outer like host membrane)
- Own circular DNA
- 70S ribosomes (bacterial type)
- Binary fission
- Size similar to bacteria
- Sensitive to antibiotics that inhibit bacteria (e.g., chloramphenicol)
- Phylogenetic analyses place mitochondria within α-proteobacteria.

Outcome:
Mitochondria enabled efficient aerobic respiration and ATP production, supporting the evolution of complex eukaryotic cells.

B. ORIGIN OF CHLOROPLASTS

Proposed event: ~1.2–1.6 billion years ago (after mitochondria)



① **Ancestral eukaryote**
A heterotrophic eukaryotic cell already containing mitochondria.

② **Engulfment**
The host cell engulfs a photosynthetic cyanobacterium.

③ **Establishment of endosymbiosis**
The cyanobacterium survives and provides photosynthate; host provides protection and nutrients.

④ **Integration**
Extensive gene transfer from cyanobacterium to host nucleus.

⑤ **Coevolution**
Endosymbiont genome reduces; specialized as a chloroplast.

⑥ **Modern chloroplast**
The endosymbiont becomes a chloroplast.

Evidence

- Double membrane (inner like bacteria, outer from host endomembrane)
- Own circular DNA
- 70S ribosomes
- Binary fission
- Size similar to cyanobacteria
- Sensitive to certain antibiotics (e.g., streptomycin)
- Phylogenetic analyses place chloroplasts within cyanobacteria.

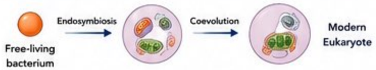
Outcome:
Chloroplasts enabled photosynthesis, leading to the evolution of photoautotrophic eukaryotes and diverse plant lineages.

COMPARISON AT A GLANCE

Feature	Mitochondria	Chloroplasts
Endosymbiont origin	α-proteobacterium	Cyanobacterium
Time of acquisition	~1.6–2.0 billion years ago	~1.2–1.6 billion years ago
Primary function	Aerobic respiration (ATP production)	Photosynthesis (light energy conversion)
Membranes	Double membrane	Double membrane
Genetic system	Circular DNA, 70S ribosomes	Circular DNA, 70S ribosomes
Mode of division	Binary fission	Binary fission
Gene transfer	Many genes to nucleus; organelle genome reduced	Extensive gene transfer to nucleus
Phylogenetic affinity	Closest to α-proteobacteria	Closest to cyanobacteria

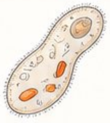
KEY POINTS

- ✓ Endosymbiosis explains the semi-autonomous nature of mitochondria and chloroplasts.
- ✓ These events represent major evolutionary innovations that increased energy efficiency and ecological range.
- ✓ Secondary and tertiary endosymbiosis (uptake of eukaryotes already containing plastids) led to the diversity of algae.



EXAMPLES

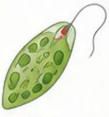
Examples showing mitochondrial endosymbiosis



Paramecium (a protozoan)

- *Paramecium*, *Amoeba*, and most animals have mitochondria for ATP production.
- Anaerobic protists (e.g., *Giardia*) have reduced mitochondria (mitosomes) reflecting secondary loss.
- *Rickettsia*-like bacteria show closest relationship to mitochondrial ancestors.

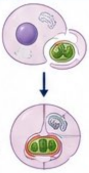
Examples showing chloroplast endosymbiosis



Euglena (a photosynthetic protozoan)

- Plants, green algae, and many protists (e.g., *Euglena*, *Chlamydomonas*) have chloroplasts for photosynthesis.
- Red algae, diatoms, and brown algae acquired plastids via secondary endosymbiosis.
- Cyanobacteria (e.g., *Anabaena*, *Nostoc*) are closest relatives of chloroplasts.

Secondary Endosymbiosis (Examples)



Eukaryote engulfs an alga

Complex plastid in dinoflagellates (e.g., *Lingulodinium*)

SUMMARY Mitochondria originated from aerobic α-proteobacteria, while chloroplasts originated from photosynthetic cyanobacteria through endosymbiosis. This partnership transformed eukaryotic cells, paving the way for multicellularity, complex life, and the oxygenation of Earth.

6 (a)

The Five–Kingdom System of Classification

(Proposed by R.H. Whittaker in 1969)

Whittaker classified all living organisms into five kingdoms—Monera, Protista, Fungi, Plantae and Animalia—on the basis of cell type, level of organization, mode of nutrition, reproduction and evolutionary relationships.

NEED FOR A NEW SYSTEM

- Earlier two-kingdom (Plantae, Animalia) system was inadequate.
- Prokaryotes and eukaryotes were not separated.
- Unicellular eukaryotes (algae, protozoa) did not fit well with plants or animals.
- Fungi were placed with plants though they are heterotrophic.
- Hence, a more natural and evolutionary system was needed.

BASIS OF FIVE–KINGDOM CLASSIFICATION

Cell structure
Prokaryotic or eukaryotic

Level of organization
Unicellular, colonial, multicellular

Mode of nutrition
Autotrophic, heterotrophic (ingestive, absorptive, saprotrophic)

Reproduction
Asexual or sexual; types of spore formation, life cycle patterns

Phylogenetic relationships
Evolutionary history and natural affinities

THE FIVE KINGDOMS – SUMMARY

1. Monera (Prokaryotes)
2. Protista (Unicellular/colonial eukaryotes)
3. Fungi (Eukaryotic, non-green, absorptive heterotrophs)
4. Plantae (Multicellular, green, autotrophs)
5. Animalia (Multicellular, ingestive heterotrophs)

CHARACTERISTICS OF THE FIVE KINGDOMS

Criteria	1. MONERA	2. PROTISTA	3. PUNGI	4. PLANTAE	5. ANIMALIA
Cell type	Prokaryotic	Eukaryotic	Eukaryotic	Eukaryotic	Eukaryotic
Level of organization	Unicellular (occasionally colonial)	Mostly unicellular; some colonial/simple multicellular	Mostly multicellular (yeast unicellular)	Multicellular	Multicellular
Cell wall	Present (peptidoglycan)	Present in some (cellulose in algae); absent in protozoa	Present (chitin)	Present (cellulose)	Absent
Mode of nutrition	Autotrophic (photo/chemo) or heterotrophic (saprophytic/parasitic)	Autotrophic (algae), heterotrophic (protozoa), mixotrophic (e.g., *Euglena*)	Heterotrophic (absorptive – saprophytes, parasites, symbionts)	Autotrophic (photosynthetic)	Heterotrophic (ingestive)
Plastids	Absent (photosynthetic pigments in membranes)	Present in algae (chloroplasts)	Absent	Present (chloroplasts with chlorophyll a & b)	Absent
Reserve food	Glycogen, poly-β-hydroxy butyrate, etc.	Starch (in algae), glycogen (in protozoa)	Glycogen, oils	Starch	Glycogen, fats
Reproduction	Asexual (binary fission, budding, fragmentation, spore formation)	Asexual (binary fission, multiple fission, budding) and sexual	Asexual (spores, budding) and sexual (various spores)	Asexual (vegetative, spores) and sexual	Predominantly sexual; asexual in some (lower animals)
Examples	Bacteria (*E. coli*, *Nostoc*), Cyanobacteria (*Anabaena*)	Amoeba, *Paramecium*, *Euglena*, *Volvox*, Diatoms	Yeast, *Rhizopus*, Mushroom (*Agaricus*), *Penicillium*	Moss, Fern, Pine, Mango, Wheat	Hydra, Earthworm, Insects, Fish, Human
Representative features	First kingdom of life; enormous diversity; found in all habitats	Bridge between prokaryotes and higher eukaryotes	Decomposers; important in nutrient cycling and symbiosis	Primary producers; form the base of food chains	Show highest level of organization, mobility and complex behaviour

KEY POINTS ABOUT THE FIVE–KINGDOM SYSTEM

- Clearly separates prokaryotes (Monera) from eukaryotes.
- Recognizes unicellular eukaryotes (Protista) as distinct from plants and animals.
- Places fungi in a separate kingdom due to heterotrophic, absorptive nutrition and chitinous cell wall.
- Considers multiple fundamental criteria and evolutionary relationships.
- Provides a natural, practical and widely accepted system for understanding biodiversity.

MERITS

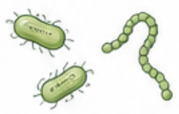
- ✓ More natural and scientific.
- ✓ Easy to understand and widely applicable.
- ✓ Reflects evolutionary relationships.
- ✓ Accommodates all major groups of organisms.
- ✓ Useful in teaching, research and biodiversity studies.

DEMERITS / LIMITATIONS

- ! Viruses and acellular forms are not included.
- ! Some organisms show mixed characters (e.g., *Euglena*).
- ! Kingdom boundaries are not always sharp.
- ! Advances in molecular biology suggest need for further refinement (three-domain/ six-kingdom systems).

DISTINGUISHING FEATURES OF THE FIVE KINGDOMS (AT A GLANCE)

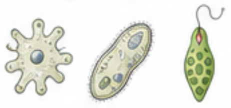
1 MONERA



Prokaryotic, unicellular

- Cell wall of peptidoglycan
- Autotrophic or heterotrophic
- Asexual reproduction
- Examples: *E. coli*, *Nostoc*

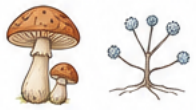
2 PROTISTA



Eukaryotic, mostly unicellular

- Algae (autotrophic), protozoa (heterotrophic), mixotrophs
- Cell wall in some
- Asexual and sexual reproduction
- Examples: *Amoeba*, *Euglena*, *Volvox*

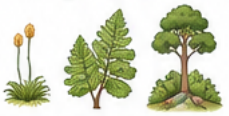
3 FUNGI



Eukaryotic, non-green

- Absorptive heterotrophs
- Cell wall of chitin
- Reproduce by spores
- Examples: Mushroom, *Rhizopus*, Yeast

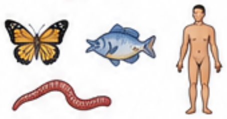
4 PLANTAE



Multicellular, green

- Photosynthetic autotrophs
- Cell wall of cellulose
- Store food as starch
- Examples: Fern, Pine, Mango

5 ANIMALIA



Multicellular, non-green

- Ingestive heterotrophs
- No cell wall
- Mostly sexual reproduction
- Examples: Insect, Fish, Human

CONCLUSION

The five-kingdom system was a major milestone in biological classification, providing a balanced and evolutionary approach to organize the living world. It laid the foundation for modern classification systems used in taxonomy and biodiversity science.

Life on Earth → Diversity → Organization → Understanding

6 (a) The Five–Kingdom System of Classification

Proposed by **R.H. Whittaker (1969)**, the five–kingdom system is based on the level of cell organization, body organization, mode of nutrition, reproduction and phylogenetic relationships.

R. H. Whittaker
(1920–1980)

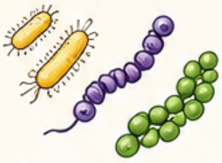
Why was it proposed?

- ✓ The earlier two-kingdom (Plantae and Animalia) system could not accommodate prokaryotes, unicellular eukaryotes and organisms with different modes of nutrition.
- ✓ It recognizes fundamental differences among organisms and reflects their evolutionary relationships.

THE FIVE KINGDOMS

① Monera
(Prokaryotes)

Unicellular prokaryotic organisms.



Key Features

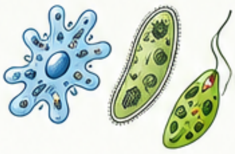
- Prokaryotic cells (no true nucleus).
- Unicellular.
- Cell wall usually present (peptidoglycan in bacteria).
- Asexual reproduction (by binary fission).
- Autotrophic (photosynthetic/chemosynthetic) or heterotrophic (saprophytic/parasitic).

Examples

Bacteria (*E. coli*, *Nostoc*), Cyanobacteria (*Anabaena*)

② Protista
(Eukaryotic unicellular)

Mostly unicellular eukaryotic organisms.



Key Features

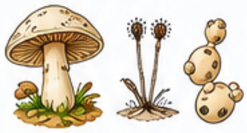
- Eukaryotic cells.
- Mostly unicellular (some colonial or simple multicellular).
- Live in aquatic or moist habitats.
- Autotrophic (algae) or heterotrophic (protozoa).
- Reproduce asexually and sometimes sexually.

Examples

Amoeba, Paramecium, Euglena, Chlamydomonas, Diatoms

③ Fungi
(Eukaryotic, non-chlorophyllous)

Eukaryotic, non-green organisms with absorptive nutrition.



Key Features

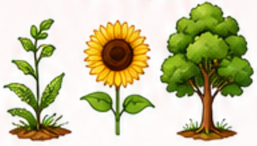
- Eukaryotic cells.
- No chlorophyll; heterotrophic (saprophytes, parasites or symbionts).
- Cell wall present (chitin).
- Body made of hyphae forming mycelium (except yeast).
- Reproduce by spores (asexual/sexual).

Examples

Mushroom (*Agaricus*), Yeast (*Saccharomyces*), Bread mould (*Rhizopus*), *Penicillium*

④ Plantae
(Multicellular, autotrophic)

Multicellular eukaryotic organisms with cell wall and chlorophyll.



Key Features

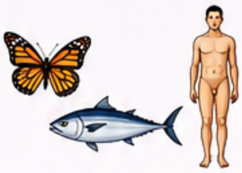
- Eukaryotic cells.
- Multicellular, well-differentiated body (tissues/organs).
- Cell wall present (cellulose).
- Autotrophic (photosynthetic).
- Store food as starch.
- Reproduce by spores and seeds/flowers (sexual & asexual).

Examples

Algae (*Spirogyra*), Moss (*Funaria*), Fern (*Pteris*), Sunflower (*Helianthus*), Mango

⑤ Animalia
(Multicellular, heterotrophic)

Multicellular eukaryotic organisms without cell wall.



Key Features

- Eukaryotic cells.
- Multicellular, well-differentiated (tissues, organs, organ systems).
- No cell wall.
- Heterotrophic; ingest food.
- Store food as glycogen.
- Mostly motile; sense organs well developed.

Examples

Insects (Butterfly), Fish (Rohu), Birds, Mammals (Human), Amphibians (Frog)

COMPARISON OF FIVE KINGDOMS

Criteria	Monera	Protista	Fungi	Plantae	Animalia
Cell Type	Prokaryotic	Eukaryotic	Eukaryotic	Eukaryotic	Eukaryotic
Body Organisation	Unicellular	Mostly unicellular	Mostly multicellular (filamentous)	Multicellular	Multicellular
Cell Wall	Present (peptidoglycan)	Present or absent (varies)	Present (chitin)	Present (cellulose)	Absent
Mode of Nutrition	Autotrophic or heterotrophic	Autotrophic or heterotrophic	Heterotrophic (absorptive)	Autotrophic (photosynthetic)	Heterotrophic (ingestive)
Reserve Food	Glycogen	Starch/Paramylon	Glycogen/Oils	Starch	Glycogen
Reproduction	Asexual (binary fission)	Asexual and sexual	Asexual and sexual (spores)	Asexual and sexual (spores, seeds)	Mostly sexual
Habitat	Everywhere	Aquatic, moist places	Moist, decaying matter, parasites	Terrestrial/aquatic	Everywhere
Examples	*E.coli, Nostoc*	Amoeba, Euglena	*Rhizopus*, Yeast	Moss, Fern, Mango	Human, Fish, Butterfly

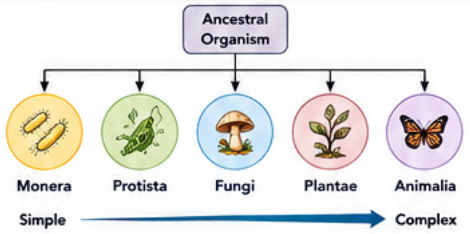
Basis of Classification

- Cell Structure
- Level of Organization
- Mode of Nutrition
- Reproduction
- Phylogenetic Relationship

Significance

- ✓ Recognizes both prokaryotic and eukaryotic organisms.
- ✓ Separates fungi from plants and prokaryotes from eukaryotes.
- ✓ Reflects – natural (evolutionary) relationships.
- ✓ Widely accepted for teaching and general use.

Evolutionary Relationship (Simplified)



Limitations

- ✗ Some protists are colonial or multicellular.
- ✗ Viruses (non-cellular) are not included.
- ✗ Bacterial cell wall composition varies.
- ✗ Boundaries between some groups are not always clear.

Quick Recall

- **Monera** – Prokaryotic, unicellular.
- **Protista** – Eukaryotic, mostly unicellular.
- **Fungi** – Eukaryotic, non-green, absorptive.
- **Plantae** – Eukaryotic, multicellular, autotrophic.
- **Animalia** – Eukaryotic, multicellular, heterotrophic.

The five–kingdom system provides a more natural, practical and evolutionary approach to classify the diversity of life based on fundamental biological differences.

6 (b)

Sympatric and Parapetric Speciation

Speciation is the evolutionary process by which new species arise from pre-existing species.
It may occur in the same geographic area (sympatric) or in adjacent areas with limited gene flow (parapetric).

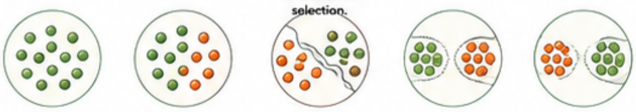
1. SYMPATRIC SPECIATION

Formation of new species from a single ancestral population while inhabiting the same geographic area.

Key idea:
Reproductive isolation evolves without any physical barrier.

How it occurs – Step by Step

1. **Ancestral population** A single species occupies a continuous habitat.
2. **Genetic variation arises** Mutations and recombination create variation within the population.
3. **Reproductive isolation evolves** Isolation may occur due to polyploidy, behavioral differences, habitat preference, temporal isolation, or disruptive selection.
4. **Gene flow stops** Individuals no longer interbreed even though they live in the same area.
5. **New species formed** Two or more reproductively isolated species coexist in the same area.



Mechanisms / Examples

- **Polyploidy:** Instant speciation in plants (e.g., new species of *Tragopogon*).
- Habitat/host shift within the same area: Apple maggot fly (*Rhagoletis pomonella*) shifted from hawthorn to apple host.
- Behavioral isolation, temporal isolation, assortative mating.
- Disruptive selection: different ecological niches within the same habitat.

Advantages

- Can occur without geographic barriers.
- Rapid speciation possible (e.g., polyploidy).

Limitations

- Requires strong disruptive forces.
- Less common in animals; more in plants and some insects.

Examples

Tragopogon (plants)

Polyploid individuals within the same area formed new species instantly.

Rhagoletis (apple maggot fly)

Host shift within same area led to reproductive isolation.

Cichlid fishes (Lake Victoria)

Diverse species evolved in the same lake due to niche differentiation and assortative mating.

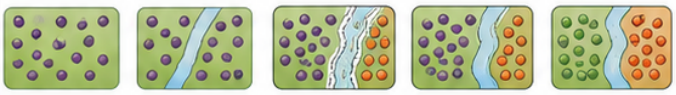
2. PARAPETRIC SPECIATION

Formation of new species from populations living in adjacent, but slightly different habitats.

Key idea:
Reproductive isolation evolves with limited gene flow across an environmental gradient.

How it occurs – Step by Step

1. **Ancestral population** A single species occupies a continuous geographic range.
2. **Population at the edge** A peripheral group encounters a different environment (e.g., climate, soil, altitude).
3. **Limited gene flow** Adjacent populations interbreed occasionally, but gene flow is restricted by distance and selection.
4. **Reproductive isolation** Differences accumulate (natural selection, genetic drift, different adaptations).
5. **New species formed** Two species coexist in adjacent habitats with a narrow contact zone.



Mechanisms / Examples

- Occurs along environmental gradients (e.g., altitude, temperature, moisture).
- Adaptations to local conditions lead to divergence.
- Narrow hybrid zone may persist.
- Often observed in plants, insects, and some vertebrates.

Advantages

- Does not require complete isolation initially.
- Gradual and common in nature.

Limitations

- Slower process; depends on strength of selection across gradient.
- Gene flow may prevent complete speciation.

Examples

Ensatina salamanders

Populations along the California coast show parapatric divergence across environmental gradients.

Certain grass species (Agrostis)

Different ecotypes occur in adjacent habitats (moist vs dry soils).

Warblers

Closely related species breed in adjacent forests with a narrow hybrid zone.

KEY DIFFERENCES – AT A GLANCE

Feature	Sympatric Speciation	Parapetric Speciation
Geographic area	Same area	Adjacent areas
Physical barrier	Absent	Partial (distance/environment)
Gene flow	Absent from the beginning (after isolation evolves)	Present but limited
Isolation mechanism	Polyploidy, ecological niche differences, behavioral, temporal, disruptive selection	Environmental gradient, natural selection, adaptation, genetic drift
Rate	Often rapid (esp, in plants)	Usually gradual
Common in	Plants, some insects, fishes	Plants, insects, some vertebrates
Example	*Tragopogon*, *Rhagoletis*, Cichlid fishes	*Ensatina salamanders*, *Agrostis*, Warblers

SIMILARITIES

- Both lead to the formation of new species.
- Both involve evolution of reproductive isolation.
- Both driven by natural selection, mutation, drift and other evolutionary forces.
- Both increase biodiversity.

IMPORTANCE

- Help explain how biodiversity arises in nature.
- Crucial in adaptive radiation and evolutionary studies.
- Provide evidence for evolution and population divergence.

Both sympatric and parapetric speciation demonstrate how new species can arise with or without strong geographic barriers, enriching life's diversity through gradual or rapid evolutionary processes.

(a)

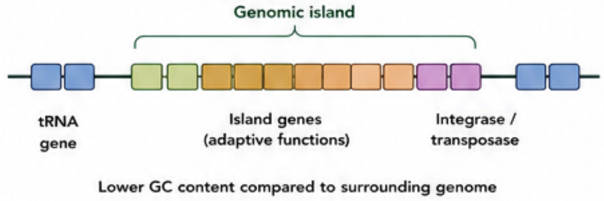
GENOMIC ISLANDS

Genomic islands (GIs) are large DNA segments in the genomes of bacteria and archaea that are acquired through horizontal gene transfer (HGT) and often provide adaptive advantages.

KEY FEATURES

- Large DNA segments (10 kb to >500 kb).
- Lower GC content than the host genome.
- Flanked by mobility genes such as integrases, transposases, tRNA genes or direct repeats.
- Often carry clusters of genes for specific functions (e.g., pathogenicity, antibiotic resistance, metabolism).
- Frequently acquired via horizontal gene transfer (HGT): transformation, transduction, or conjugation.
- Not essential for basic survival but provide selective advantages in specific environments.

TYPICAL ORGANIZATION


Genomic island
tRNA gene
Island genes (adaptive functions)
Integrase / transposase
Lower GC content compared to surrounding genome

COMMON GENES FOUND IN GENOMIC ISLANDS

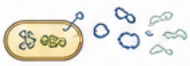
- Antibiotic resistance
- Bacteriocin production
- Virulence factors
- Metabolic pathways
- Secretion systems
- Motility and adaptation

IMPORTANCE

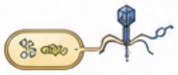
- Promote rapid evolution and genomic plasticity.
- Contribute to virulence and survival in hostile environments.
- Play key role in the emergence of antibiotic resistance.
- Help in niche adaptation and speciation.
- Important in biotechnology (e.g., novel enzymes, metabolic pathways).

ORIGINS / ACQUISITION (HORIZONTAL GENE TRANSFER)

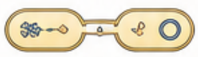
Transformation
Uptake of free DNA from the environment.



Transduction
Transfer of DNA by bacteriophages (viruses).



Conjugation
Transfer of DNA via plasmids or conjugative elements.



EXAMPLES

- *Salmonella* Pathogenicity Island 1 (SPI-1): carries genes for type III secretion system; invasion of host cells.
- Pathogenicity Island 2 (SPI-2) in *Salmonella*: intracellular survival.
- *Vibrio cholerae* CTXφ (pathogenicity island): cholera toxin genes.
- *Escherichia coli* Pathogenicity Islands (e.g., PAI I536): iron acquisition, toxin production.
- Many genomic islands in *Bacillus, Pseudomonas, Yersinia* etc. encode virulence and resistance traits.

DETECTION OF GENOMIC ISLANDS

- GC content deviution analysis.
- Presence of mobility genes (integrases, transposases, tRNA genes).
- Codon usage bias different from host genome.
- Comparative genomics (presence in some strains but absent in others).
- Bioinformatics tools: IslandViewer, SIGI-HMM, IslandPath-DIMOB, etc.

(b)

HISTORY OF EVOLUTION OF *HOMO SAPIENS*

Humans evolved from early primates through a long process of gradual changes in body structure, brain capacity, culture and behaviour.

Time (approx.)	Species / Stage	Key Features	Major Fossil / Evidence	Geographical Distribution	Illustration
6–8 million years ago	**Early Hominin** *(Sahelanthropus tchadensis, Orrorin tugenensis)*	• Bipedal tendencies begin. • Foramen magnum forward positioned.	Toumai (*Sahelanthropus*), Orrorin fossils	Africa (Central, East)	Early hominin (skeletal remains)
4.4–2 million years ago	**Australopithecines** *(Australopithecus afarensis, A. africanus)*	• Fully bipedal. • Brain ~ 400–550 cc. • Thin body, long arms.	"Lucy" (*A. afarensis*), Taung Child (*A. africanus*)	Africa (East, South)	*Australopithecus afarensis*
2.4–1.4 million years ago	**Homo habilis**	• Brain ~ 600–700 cc. • First stone tools (Oldowan). • Less prognathous face.	KNM-ER 1813, OH 24 (skull & tools)	Africa (East)	*Homo habilis*
1.8–0.3 million years ago	**Homo erectus** (including *H. ergaster*)	• Brain ~ 800–1100 cc. • Well-built body; long-distance walker/runner. • Acheulean tools; use of fire.	Java Man (*Pithecanthropus erectus*), Turkana Boy	Africa, Asia (Java, China, West Asia)	*Homo erectus* (Java Man)
400,000–40,000 years ago	**Homo heidelbergensis** (Archaic humans)	• Brain ~ 1100–1400 cc. • Advanced hunting; shelters. • Ancestor of Neanderthals and modern humans.	Heidelberg jaw, Kabwe skull	Africa, Europe, West Asia	*Homo heidelbergensis*
400,000–40,000 years ago	**Homo neanderthalensis**	• Robust body; adapted to cold. • Brain ~ 1200–1600 cc. • Burials; use of tools, fire; possible language.	Neander Valley fossils (Germany)	Europe, West Asia	Neanderthal man
~300,000 years ago–present	**Homo sapiens** (Modern humans)	• Brain ~ 1350 cc (avg). • Complex language, art, culture. • Advanced tools, agriculture, civilization.	Cro-Magnon fossils, Jebel Irhoud (Morocco), Omo Kibish (Ethiopia)	Origin in Africa; now worldwide	Modern human

MAJOR TRENDS IN HUMAN EVOLUTION

- ✓ Increase in brain size and cranial capacity.
- ✓ Shift from arboreal to bipedal life.
- ✓ Reduction in body hair, jaws and teeth size.
- ✓ Development of tools, culture, language and art.
- ✓ Expansion from Africa to all parts of the world.

OUT OF AFRICA (MODERN HUMAN DISPERSAL)

Modern humans evolved in Africa (~300,000 years ago) and dispersed in waves:

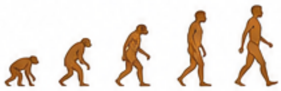
- ~70,000–60,000 years ago → Middle East, Asia, Australia
- ~50,000 years ago → Europe
- ~15,000–12,000 years ago → Americas

Interbreeding occurred with Neanderthals and Denisovans in Eurasia.

SIGNIFICANCE

- ★ Shows a gradual, branching evolution.
- ★ Highlights the importance of adaptation, culture and environment.
- ★ Explains our shared ancestry with other primates.
- ★ Helps understand human diversity and unity.

From simple beginnings in Africa to the intelligent, creative and socially complex *Homo sapiens*—human evolution is a remarkable story of life's journey through time.



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उपन अपन अनविरसीय

INDIRA GANDHI NATIONAL OPEN UNIVERSITY
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ODISHA CBZ ZONE

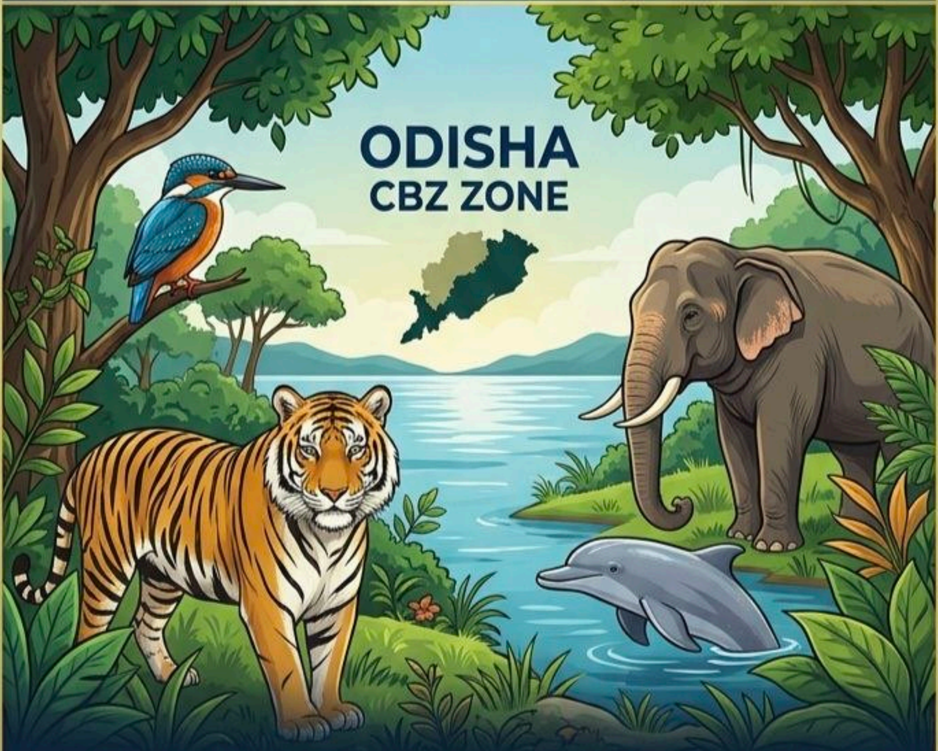
MZO 04

IGNOU MSc ZOOLOGY

PREVIOUS YEAR QUESTIONS (PYQs)

DECEMBER 2024 TERM END EXAMINATION

WITH ODISHA CBZ ZONE



TERM END EXAMINATION (TEE): DEC 2024
SUBJECT: ZOOLOGY (MSC)

No. of Printed Pages : 3 **MZO–004**

M. SC. (ZOOLOGY)

(MSCZOO)

Term-End Examination

December, 2024

MZO-004 : SYSTEMATICS, BIODIVERSITY AND EVOLUTION

Time : 2 Hours *Maximum Marks : 50*

Note : (*i*) *Attempt any **five** questions.*

(*ii*) *All questions carry equal marks.*

---

1. Explain the fundamental principles of evolution that are the foundations of modern evolutionary biology. 10

2. Describe the theory of spontaneous generation. Discuss the Urey-Miller experiment and its conclusion. 5+5=10

3. (a) What is a phylogenetic tree ? Explain the key points about the phylogenetic tree with suitable examples. 5

   (b) How will you construct phylogenetic tree by using 16S rRNA gene sequence ? 5

4. What is molecular clock ? Explain its calibration with suitable examples. 10

5. Write short notes on the following : 5×2=10

   (a) Evolution of eukaryotic genome

   (b) Secondary and tertiary endosymbiosis

6. Describe the molecular and genetic basis of speciation. 10

7. Describe the following : 5×2=10

   (a) Recent trends in human evolution

   (b) Consequences of horizontal gene transfer in bacteria

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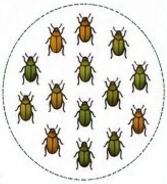
FUNDAMENTAL PRINCIPLES OF EVOLUTION

THE FOUNDATION OF MODERN EVOLUTIONARY BIOLOGY

Evolution is the change in heritable characteristics of biological populations over generations.
These core principles explain how and why evolution happens.

1 POPULATIONS, NOT INDIVIDUALS, EVOLVE

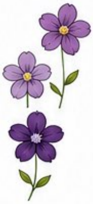
- Evolution acts on populations, which are groups of interbreeding individuals of the same species living in the same area.
- Individuals can adapt, but evolution is a change in the genetic makeup (allele frequencies) of the population.



Example: A population of beetles may change in color over time, not a single beetle.

2 HERITABLE VARIATION EXISTS

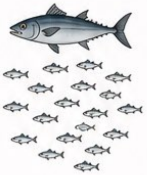
- Individuals in a population vary in their traits due to genetic differences.
- Variation arises from mutations, genetic recombination (sexual reproduction) and gene flow.
- Only heritable variations can be passed to offspring.



Example: Flower color variation in a population is due to different alleles.

3 OVERPRODUCTION OF OFFSPRING

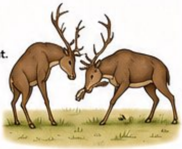
- Organisms produce more offspring than can survive to reproduce.
- This leads to competition for limited resources such as food, space, mates and shelter.



Example: A female fish may produce thousands of eggs, but only a few survive.

4 STRUGGLE FOR EXISTENCE

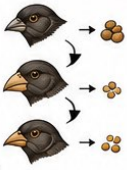
- Because resources are limited, individuals compete with others and with the environment.
- Struggle can be intraspecific (within the same species) or interspecific (between different species).



Example: Male deer compete for mates; not all succeed in reproducing.

5 NATURAL SELECTION

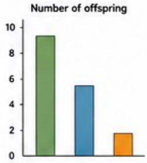
- Individuals with traits that give them an advantage survive and reproduce more.
- Those with less advantage leave fewer offspring.
- Natural selection is "survival and reproduction of the fittest.



Example: Finches with stronger beaks may survive better during droughts and pass on those traits.

6 DIFFERENTIAL REPRODUCTIVE SUCCESS

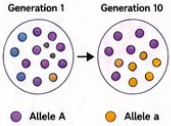
- The environment "chooses which individuals leave more offspring.
- Fitness is not absolute strength, but the ability to leave the most viable offspring in a given environment.



Example: In a dry year, drought-tolerant plants produce more seeds.

7 CHANGE IN ALLELE FREQUENCIES OVER TIME

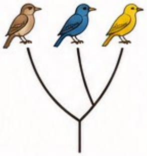
- Evolution is a change in the frequency of alleles in a population across generations.
- Favorable alleles increase; unfavorable alleles decrease.



Example: Over generations, the frequency of allele A increases in the population.

8 SPECIATION

- New species arise from existing species when populations become reproductively isolated.
- Isolation can be geographical, ecological, behavioral or genetic.



Example: Darwin's finches evolved into different species adapted to different niches.

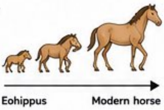
9 COMMON ANCESTRY

- All organisms are descended from one or a few common ancestors.
- This is supported by fossil record, comparative anatomy, embryology and molecular data.

Example: Humans and chimpanzees share a common ancestor.

10 EVOLUTION IS GRADUAL OVER LONG PERIODS

- Evolution occurs over many generations, usually too slow to be seen in a single lifetime.
- Small changes accumulate over long periods to produce large differences.



Example: Horses evolved from small, multi-toed ancestors over millions of years.

11 EVOLUTION IS CONTINGENT AND NON-TELEOLOGICAL

- Evolution has no goal or predetermined direction.
- It depends on chance events (mutations, drift, environment).
- Adaptations are historical outcomes, not perfect solutions.

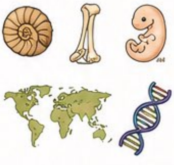
ADAPTATION A
ADAPTATION B

Example: Different environments can lead to different adaptations.

12 EVIDENCE SUPPORTS EVOLUTION

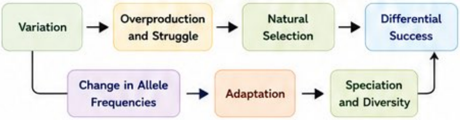
Evolution is supported by multiple lines of converging evidence:

- ✓ Fossil record
- ✓ Comparative anatomy
- ✓ Embryology
- ✓ Biogeography
- ✓ Molecular biology
- ✓ Direct observation



Example: Transitional fossils show gradual change connecting major groups.

HOW THESE PRINCIPLES WORK TOGETHER



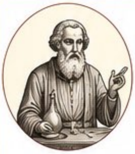
Variation → Overproduction and Struggle → Natural Selection → Differential Success

Change in Allele Frequencies → Adaptation → Speciation and Diversity

IN SUMMARY

These fundamental principles explain how life on Earth diversified from simple beginnings into the vast variety we see today. They form the theoretical framework of modern evolutionary biology and are supported by evidence from many scientific disciplines.

Key Take-home Message: Evolution is a natural, evidence-based process that explains the unity and diversity of life. It is driven by variation, natural selection and heredity, acting over time on populations.



ORIGIN OF LIFE: SPONTANEOUS GENERATION & UREY–MILLER EXPERIMENT

Two important ideas about the origin of life:
(1) Spontaneous Generation – early belief that life arises from non-living matter.
(2) Urey–Miller Experiment – modern scientific test showing how organic molecules can form under prebiotic conditions.

1. THEORY OF SPONTANEOUS GENERATION

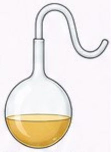
The theory of **spontaneous generation** proposes that living organisms can **arise directly from non-living matter** under natural conditions.

KEY PROPOSITIONS

- Life originated many times independently from non-living substances.
- Simple organisms could arise from decaying matter, mud, water, sweat, etc.
- No life or pre-existing life is required for the origin of a new organism.

HISTORICAL BACKGROUND

- Ancient Greeks (Aristotle) believed frogs came from mud, mice from grain, insects from decaying matter.
- This view persisted for centuries.
- Needham (1745): Boiled broth left in open vessel developed microorganisms; he concluded life arose spontaneously.
- Spallanzani (1768): Boiled broth sealed in flask showed no growth; argued that life comes from existing life.
- Pasteur (1861): Swan-neck flask experiment definitively disproved spontaneous generation.



Swan-neck flask experiment

EXAMPLES EARLY BELIEVERS GAVE

Maggots from decaying meat

Mice from grain

Frogs from mud

Microorganisms from putrefying broth

STATUS TODAY

- Spontaneous generation is rejected by modern science.
- Life arises only from pre-existing life (Biogenesis).
- However, the idea that life can arise from non-living chemicals (evolution of life by chemical processes) is still investigated.

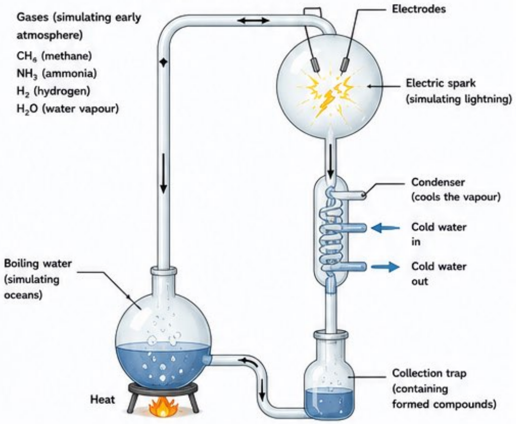
SPONTANEOUS GENERATION: SUMMARY

Aspect	Details
Proposed by	Ancient philosophers; Needham (1745)
Core idea	Life arises from non-living matter spontaneously
Examples	Maggots from meat, mice from grain, etc.
Major challenge	Contradicted observations (Spallanzani, Pasteur)
Modern view	Disproved; life comes from pre-existing life

2. UREY–MILLER EXPERIMENT

The Urey–Miller experiment (1953) tested the hypothesis that organic molecules could form from simple inorganic substances under conditions similar to early Earth.

EXPERIMENTAL SETUP

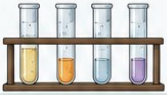

Gases (simulating early atmosphere)
CH_6 (methane)
NH_3 (ammonia)
H_2 (hydrogen)
H_2O (water vapour)
Electrodes
Electric spark (simulating lightning)
Condenser (cools the vapour)
Cold water in
Cold water out
Boiling water (simulating oceans)
Heat
Collection trap (containing formed compounds)

PROCEDURE

1. Water was boiled to produce steam.
2. A mixture of gases (CH_4, NH_3, H_2, H_2O) was circulated.
3. Electric sparks were passed for about one week (simulating lightning).
4. The vapours were cooled; products collected in the trap.
5. The contents were analysed for organic compounds.

RESULTS

Amino acids (e.g., glycine, alanine), urea, lactic acid, and other molecules were formed.



CONCLUSION

- ✓ Simple inorganic molecules can be converted into organic molecules under conditions resembling early Earth.
- ✓ This supports the chemical evolution theory – life may have originated through a gradual chemical process.
- ✓ However, the experiment did not produce life or self-replicating molecules.
- ✓ It shows that the building blocks of life can form naturally, but the origin of life involves further steps (polymerization, protocells, etc.).

UREY–MILLER EXPERIMENT: SUMMARY

Aspect	Details
Proposed by	Stanley L. Miller (with Harold Urey), 1953
Purpose	To simulate early Earth and test chemical evolution
Conditions	Reducing atmosphere + lightning + water
Outcome	Formation of amino acids and other organics
Significance	Supports abiotic synthesis of life's building blocks

KEY TAKE-HOME MESSAGE

Spontaneous generation is a disproven idea. The Urey–Miller experiment showed that while life does not arise spontaneously as organisms, the building blocks of life can form naturally under early Earth conditions.

PHYLOGENETIC TREE

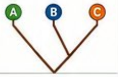
• The Tree of Life •

A phylogenetic tree (or evolutionary tree or cladogram) is a branching diagram that shows the evolutionary relationships among organisms or genes based on shared characteristics and common ancestry.

KEY POINTS ABOUT PHYLOGENETIC TREE

1 Shows evolutionary relationships, not a sequence

It shows how species are related through common ancestry, not a progression from primitive to advanced.

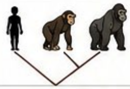


2 Built from characters (morphological or molecular)

Trees are reconstructed using shared derived characters from morphology, DNA, RNA or protein sequences.

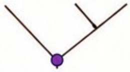
3 Terminal taxa (tips)

The tips (end points) represent existing species or genes being compared.



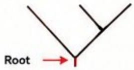
4 Internal nodes (branch points)

Each node represents a common ancestor from which descendant lineages diverge.



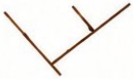
5 Root

The base of the tree indicates the most recent common ancestor of all taxa shown.



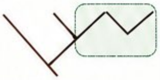
6 Branches (lineages)

Branches represent lineages. The length of branches may indicate amount of change or genetic distance (in some trees).



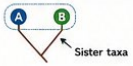
7 Clades

A clade includes an ancestor and all of its descendants. It is a natural (monophyletic) group.



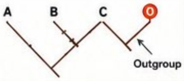
8 Sister taxa

Two taxa that share an immediate common ancestor are called sister taxa.


A
B
Sister taxa

9 Outgroup

An outgroup is a taxon outside the group of interest used to root the tree and infer the direction of evolution.


A
B
C
O
Outgroup

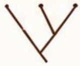
10 Hypothesis-based

Phylogenetic trees are hypotheses of relationships and can change with new data and better methods.

TYPES OF PHYLOGENETIC TREES

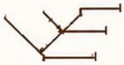
1. Cladogram (most common)

Shows branching order of lineages based on shared derived characters. Does not show the amount of change.



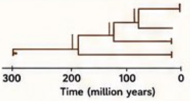
2. Phylogram

Branch lengths are proportional to the amount of evolutionary change or genetic distance.



3. Chronogram

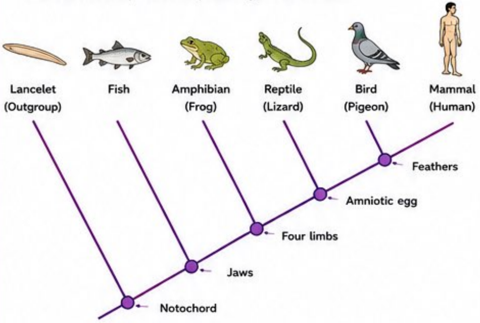
Branch lengths are proportional to time. Shows when lineages diverged.


300
200
100
0
Time (million years)

EXAMPLES OF PHYLOGENETIC TREES

A. Example 1: Vertebrates (based on morphology and molecules)

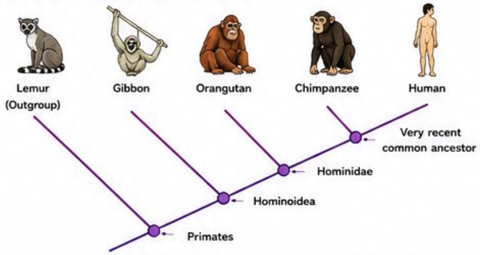
Shows evolutionary relationships among five vertebrates.


Lancelet (Outgroup)
Fish
Amphibian (Frog)
Reptile (Lizard)
Bird (Pigeon)
Mammal (Human)
Feathers
Amniotic egg
Four limbs
Jaws
Notochord

Interpretation: Birds and mammals are more closely related to each other (share a more recent common ancestor) than to reptiles or amphibians.

B. Example 2: Primates (based on DNA sequences)

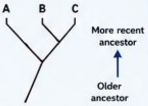
Shows relationships among selected primates.


Lemur (Outgroup)
Gibbon
Orangutan
Chimpanzee
Human
Very recent common ancestor
Hominidae
Hominoidea
Primates

Interpretation: Humans and chimpanzees are sister taxa and share a very recent common ancestor.

HOW TO READ A PHYLOGENETIC TREE

- Read from the base (root) towards the tips.
- Taxa that join at a node share a common ancestor.
- The closer the node connecting two taxa to the tips, the more closely related they are.
- Trees do not imply "higher" or "lower" organisms.


A
B
C
More recent ancestor
Older ancestor

IMPORTANCE / APPLICATIONS

- Reconstructs evolutionary history and relationships.
- Helps in classification and understanding biodiversity.
- Used in comparative genomics and molecular evolution.
- Important in epidemiology (tracking evolution of pathogens).
- Guides conservation by identifying evolutionary distinct lineages.
- Useful in forensic science and legal studies.

IN SUMMARY. A phylogenetic tree is a visual representation of evolutionary relationships based on common ancestry. It is a powerful tool that helps us understand the diversity of life and its history on Earth.

CONSTRUCTING A PHYLOGENETIC TREE
USING 16S rRNA GENE SEQUENCE

16S rRNA gene is present in all bacteria and archaea.
It has conserved regions (for universal primers) and variable regions (for distinguishing taxa).
Therefore, it is widely used for reconstructing evolutionary relationships.

STEP-BY-STEP WORKFLOW

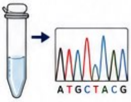
1 Sample collection and DNA extraction

- Collect bacterial samples from the environment, clinical or cultured isolates.
- Extract total genomic DNA from each sample.

2 PCR amplification of 16S rRNA gene

- Use universal primers (e.g., 27F and 1492R) to amplify ~1.5 kb 16S rRNA gene.
- Verify PCR product on agarose gel.

3 Purification and sequencing



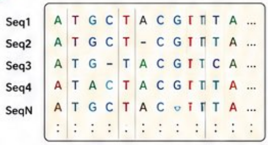
- Purify PCR product to remove primers and dNTPs.

Sequence the PCR product (Sanger targeted sequencing or NGS).

4 Sequence editing and quality check

- Check raw reads and trim low-quality ends.
- Assemble forward and reverse reads to get high-quality consensus 16S rRNA sequence.

5 Multiple sequence alignment


Seq1 A T G C T A C G T T T A ...
Seq2 A T G C T - C G T T T A ...
Seq3 A T G - T A C G T T C A ...
Seq4 A T A C T A C G T T T A ...
SeqN A T G C T A C G T T T A ...

- Align all 16S rRNA gene sequences using software (e.g., MAFFT, Clustal Omega, MUSCLE).
- Alignment arranges homologous nucleotides in the same columns.

6 Model selection

Determine the best-fit model of nucleotide substitution (e.g., using jModelTest, ModelFinder).

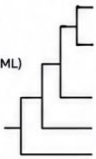
Model	AIC score	Selected?
JC69	2567.3	No
K2P	2145.8	No
GTR+G	1932.6	Yes

The best model is used for tree inference.

7 Phylogenetic tree construction

Infer the tree using suitable method:

- Distance-based: Neighbor-Joining (NJ) (e.g., using MEGA)
- Character-based: Maximum Likelihood (ML) (e.g., IQ-TREE, RAxML)
- Bayesian Inference (e.g., MrBayes)

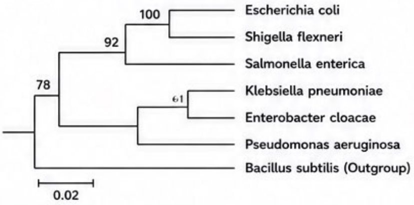


Methods use the alignment and model to reconstruct evolutionary relationships.

8 Tree evaluation and interpretation

Assess reliability of the tree using bootstrap analysis (usually 500–1000 replicates). Bootstrap values (shown at nodes) indicate support (>70% = good support).

EXAMPLE PHYLOGENETIC TREE (Neighbor-Joining)



Interpretation:

- E. coli and Shigella are very closely related (bootstrap 100).
- Salmonella is sister to the E. coli–Shigella clade.
- Klebsiella and Enterobacter form another clade.
- Pseudomonas is more distant.
- Bacillus (outgroup) roots the tree.

Rooting: Use an appropriate outgroup (a distantly related sequence).

COMMON TOOLS

Sequence retrieval	NCBI GenBank, SILVA, RDP
Alignment	MAFFT, Clustal Omega, MUSCLE
Model selection	jModelTest, ModelFinder
Tree construction	MEGA (NJ/ML), IQ-TREE, RAxML, MrBayes
Tree visualization	FigTree, iTOL, MEGA

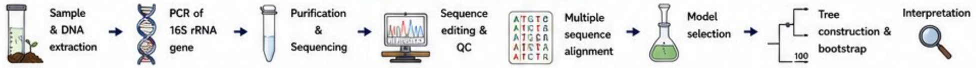
IMPORTANT CONSIDERATIONS

- Use high-quality, nearly full-length 16S sequences (~1,300–1,500 bp) for better resolution.
- Remove chimeric sequences (check using tools like UCHIME, VSEARCH).
- Ensure good alignment; poorly aligned regions can mislead trees.
- 16S rRNA is excellent for identifying bacteria/archaea at genus level; may not resolve very closely related species.
- Combine 16S with other genes or whole-genome data for higher resolution.

APPLICATIONS

- Identification of unknown bacteria
- Taxonomy and classification
- Microbial diversity studies (environmental/clinical)
- Evolutionary and ecological studies
- Discovery of novel taxa

SUMMARY OF THE PROCESS



Sample & DNA extraction → PCR of 16S rRNA gene → Purification & Sequencing → Sequence editing & QC → Multiple sequence alignment → Model selection → Tree construction & bootstrap → Interpretation

KEY TAKE-HOME MESSAGE The 16S rRNA gene provides a universal molecular marker for inferring evolutionary relationships among bacteria and archaea. By amplifying, sequencing, aligning and analyzing 16S rRNA gene sequences, we can construct phylogenetic trees that reveal their evolutionary history.

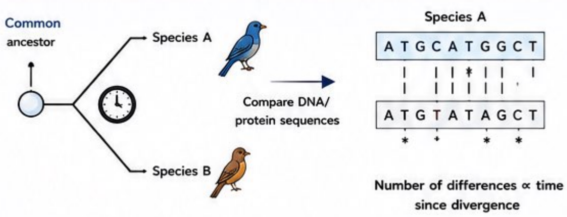
MOLECULAR CLOCK

The molecular clock is the hypothesis that genetic mutations accumulate at a relatively constant rate over time. By comparing genetic differences between species or genes, we can estimate the time of evolutionary events in the past.

KEY CONCEPTS

- Mutations occur during DNA replication and are passed to the next generation.
- If the mutation rate is approximately constant, the number of differences between two lineages is proportional to the time since they diverged.
- Molecular clocks can be applied to DNA or protein sequences.
- Rates vary among genes and lineages; therefore, calibration is essential for accurate dating.

HOW IT WORKS



Common ancestor

Species A

Species B

Compare DNA/ protein sequences

Species A

A T G C A T G G C T

A T G T A T A G C T

* * * *

Number of differences ∝ time since divergence

CALIBRATION OF MOLECULAR CLOCK

Calibration converts genetic distance (substitutions per site) into absolute time (years).
It provides a known rate or time point to scale the molecular clock.

CALIBRATION METHODS

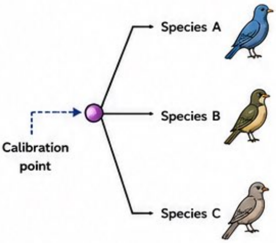
1 Fossil Calibration (most common)

- Fossils provide a minimum age for a node in the tree.
- The divergence cannot be more recent than the fossil age.
- Used as a constraint to estimate substitution rate or divergence time.

2 Geological/Geochemical Calibration

- Events such as island formation, mountain uplift, or ocean opening are dated geologically.
- Used when fossils are not available for a lineage.

HOW CALIBRATION WORKS (Example)



Species A

Species B

Species C

Calibration point

Suppose the fossil record shows that Species B and C diverged at least 20 million years ago (calibration point).

Observed genetic distance between B and C = 0.10 (substitutions per site)

Rate = 20 Myr / 0.10 = 200 Myr per substitution per site

If genetic distance between A and B = 0.15, then

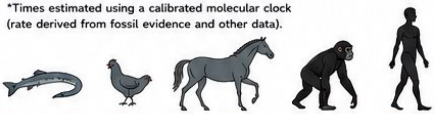
Divergence time (A–B) = 0.15 × 200 = 30 million years ago

EXAMPLE 1: CYTOCHROME c IN VERTEBRATES

The cytochrome c protein is highly conserved.
Pairwise differences are used to infer divergence times.

Species Pair	No. of Amino Acid Differences	Estimated Divergence Time (Million Years Ago)*
Human – Chimpanzee	0	5 – 7
Human – Horse	12	50 – 60
Human – Chicken	19	300 – 310
Human – Lamprey	25	500

*Times estimated using a calibrated molecular clock (rate derived from fossil evidence and other data).

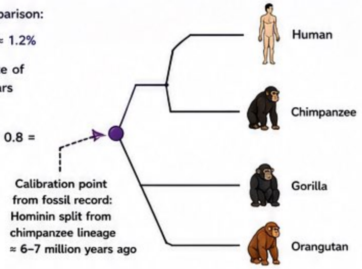


EXAMPLE 2: HUMAN–CHIMPANZEE SPLIT USING DNA

Mitochondrial DNA comparison:

- Sequence difference ≈ 1.2%
- Using a calibrated rate of ~0.8% per million years

Divergence time ≈ 1.2 / 0.8 = 1.5 million years ago



Human

Chimpanzee

Gorilla

Orangutan

Calibration point from fossil record: Hominin split from chimpanzee lineage ≈ 6–7 million years ago

IMPORTANT CONSIDERATIONS

- ✓ Mutation rates are not identical for all genes or lineages.
- ✓ Use multiple genes/regions for reliable estimates.
- ✓ Relaxed molecular clock models allow rate variation among lineages.
- ✓ Always combine molecular data with fossil, and biogeographic evidence.

APPLICATIONS

- Estimate timing of speciation, adaptation and evolutionary events.
- Reconstruct evolutionary history.
- Track evolution of pathogens (e.g., viruses, bacteria).
- Study biogeography and timing of dispersal events.

SUMMARY

The molecular clock uses the steady accumulation of genetic changes as a natural "clock" to measure Evolutionary time. Calibration with fossils or geological events translates genetic differences into real time, enabling us to date key events in the history of life.

KEY TAKE-HOME MESSAGE

The molecular clock turns genetic differences into time. Calibration with fossils or geological events provides the scale needed to unlock the timing of evolution.

SHORT NOTES ON

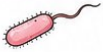
(a) EVOLUTION OF EUKARYOTIC GENOME

Eukaryotic genomes are more complex than prokaryotic genomes in size, organization and regulation. They evolved through a combination of endosymbiosis, gene duplication, horizontal gene transfer (HGT), intron gain and genome rearrangements.

KEY STEPS IN THE EVOLUTION OF EUKARYOTIC GENOME

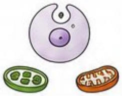
1 Origin from prokaryotic ancestor

The last universal common ancestor (LUCA) was a prokaryote with a small genome.



2 Endosymbiotic acquisition

An ancestral host cell engulfed an aerobic α-proteobacterium (→ mitochondrion) and a cyanobacterium (→ chloroplast in plants and algae).

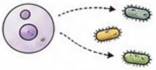


3 Increase in genome size

Gene duplication, transposons, introns and non-coding DNA contributed to genome expansion.

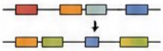
4 Horizontal gene transfer (HGT)

Genes were acquired from bacteria, archaea, viruses and organelles, providing new functions.



5 Rearrangements and regulatory innovation

Chromosomal rearrangements, alternative splicing, new promoters and epigenetic mechanisms refined gene regulation.



6 Compartmentalization and specialization

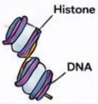
Genome evolution was linked with the rise of nucleus, cytoskeleton, endomembrane system and multi-cellularity.

OUTCOME

Eukaryotic genomes became large (10^7 – 10^{11} bp), rich in non-coding sequences, introns and repetitive elements, and capable of complex regulation and diversity of life.

FEATURES OF EUKARYOTIC GENOME

- Linear chromosomes associated with histone proteins.
- Presence of introns, exons and large non-coding regions.
- Gene families formed by duplication.
- Repetitive DNA: transposons, retroelements, satellite DNA.
- Dynamic genome with gene gain, loss and rearrangements.



SOURCES OF GENOMIC INNOVATION

Gene duplication	Creates new genes that evolve new functions.
Horizontal gene transfer	Acquisition of genes from distantly related organisms.
Transposable elements	Cause insertions, deletions and regulatory changes.
Intron gain and alternative splicing	Increase protein diversity from the same gene.
Whole genome duplication (polyploidy)	Common in plants, fungi and some protists; promotes complexity.

EXAMPLES

- Yeast (*Saccharomyces cerevisiae*) genome ~12 Mb with ~6,000 genes.
- Human genome ~3.2 Gb with ~20,000 protein-coding genes but large non-coding portion (~98%).
- Many eukaryotic genes have mixed ancestry (from bacterial, archaeal, viral and eukaryotic sources).

SIGNIFICANCE

- Explains origin of complex cellular structure and functions.
- Provides raw material for evolution of new traits.
- Basis of adaptation, development and speciation.
- Helps in understanding evolution of gene families and metabolic pathways.

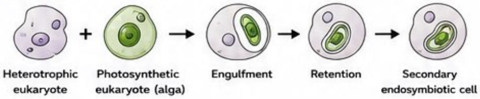
(b) SECONDARY AND TERTIARY ENDOSYMBIOSIS

Endosymbiosis is the process by which one cell lives inside another cell in a mutually beneficial relationship. While primary endosymbiosis (origin of mitochondria and chloroplasts) occurred early in eukaryotic evolution, secondary and tertiary endosymbiosis explain the origin of complex plastids in some algae.

SECONDARY ENDOSYMBIOSIS

A eukaryotic cell engulfs another eukaryotic photosynthetic cell (alga) and retains it as a plastid.

PROCESS



EXAMPLES

- Dinoflagellates (e.g., *Peridinium, Alexandrium*): plastids with 2–4 membranes.
- Diatoms and brown algae (e.g., *Phaeodactylum, Ectocarpus*): plastids with 4 membranes.
- Euglenids (euglenophytes): plastids with 3 membranes.

KEY FEATURES

✓ Plastids are surrounded by 3 or 4 membranes.
Presence of a "nucleomorph" (reduced algal nucleus) in many lineages.
✓ Most plastid-targeted proteins are encoded by the host nucleus, not by the engulfed alga.

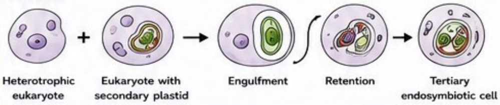
SIGNIFICANCE

- Explains diversity of plastids beyond those derived from cyanobacteria.
- Shows that complex organelles can arise repeatedly through symbiosis.
- Important in evolution of marine phytoplankton and protists.

TERTIARY ENDOSYMBIOSIS

A eukaryotic cell with a secondary plastid is engulfed by another eukaryotic cell and retained as a plastid.

PROCESS



EXAMPLES

- Cryptophytes (e.g., *Guillardia, Cryptomonas*): plastids with 3–4 membranes.
- Some Haptophytes.

KEY FEATURES

✓ Plastids typically have 3 or 4 membranes (derived from the plastid of the secondary **endosymbiont**).
✓ Nucleomorph usually absent or highly reduced.
✓ Even more genes transferred to the host nucleus.

SIGNIFICANCE

- Explains the presence of highly complex plastids in some protists.
- Demonstrates multiple, independent endosymbiotic events in evolution.
- Broadens our understanding of organelle evolution and diversity.

IN SUMMARY

- Eukaryotic genome evolved by endosymbiosis, gene duplication, HGT, intron gain and genome rearrangements, leading to complexity and diversity.
- Secondary and tertiary endosymbiosis produced complex plastids in many algal lineages, highlighting the dynamic role of symbiosis in evolution.

MOLECULAR AND GENETIC BASIS OF SPECIATION

Speciation is the evolutionary process by which new species arise from existing species through the evolution of reproductive isolation. Molecular and genetic changes generate and reinforce this isolation.

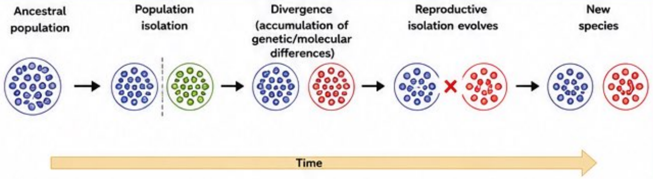
1. WHAT IS SPECIATION?

Formation of new species from a common ancestor. Requires the evolution of reproductive isolation between diverging populations.

Types:

- **Allopatric** – geographic isolation
- **Sympatric** – without geographic isolation
- **Parapatric** – adjacent populations with limited gene flow
- **Peripatric** – small isolated population at the edge of range

2. OVERALL PROCESS (FROM POPULATION TO SPECIES)



Ancestral population → Population isolation → Divergence (accumulation of genetic/molecular differences) → Reproductive isolation evolves → New species

3. MOLECULAR AND GENETIC BASIS OF SPECIATION

3.1 SOURCES OF GENETIC AND MOLECULAR VARIATION

Mutations
Point mutations, insertions, deletions, inversions, translocations, copy number changes create new alleles.

Recombination
Crossing over, independent assortment and gene conversion create new allele combinations.

Gene duplication
Provides raw material for evolution of new genes and functions (neofunctionalization, subfunctionalization, pseudogenization).

Transposable elements
Promote mutations, gene regulation changes and genome rearrangements.

3.2 MECHANISMS DRIVING MOLECULAR DIVERGENCE

- **Genetic drift**
  Random change in allele frequencies, strong in small, isolated populations.

Change by chance

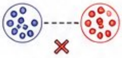
- **Natural selection**
  Different environments favor different alleles; adaptive divergence.

Different selection

- **Mutation**
  Introduces novel alleles that may be neutral, beneficial or deleterious.

A → G

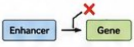
- **Gene flow (reduced or absent)**
  Limited gene exchange allows divergence to accumulate.



Reduced gene flow

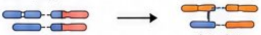
3.3 GENOMIC CHANGES IMPORTANT IN SPECIATION

- Accumulation of nucleotide substitutions in coding and non-coding regions.
- Changes in gene regulation (promoters, enhancers, silencers, miRNAs, epigenetic marks).



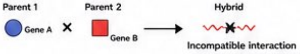
Regulatory change

- Chromosomal rearrangements: inversions, translocations, fusions/fissions reduce recombination in heterokaryotypes.



Inversion

- Hybrid incompatibility genes evolve (Dobzhansky–Muller incompatibilities).



Incompatible interaction → reduced fitness or sterility

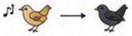
- Polyploidy (especially in plants) – instant reproductive isolation and novel gene dosage effects.

4. MOLECULAR BASIS OF REPRODUCTIVE ISOLATION

4.1 PREZYGOTIC ISOLATION

Prevent mating or fertilization.

- **Behavioral isolation:** differences in courtship signals (songs, dances, pheromones).



- **Temporal isolation:** breeding at different times.

- **Habitat/ecological isolation:** different habitats or hosts.

- **Mechanical isolation:** differences in reproductive structures.

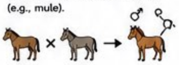
- **Gametic isolation:** sperm–egg incompatibility.

4.2 POSTZYGOTIC ISOLATION

Occurs after fertilization.

- **Reduced hybrid viability:** hybrids die early.

- **Reduced hybrid fertility:** hybrids survive but are sterile (e.g., mule).



- **Hybrid breakdown:** F1 viable and fertile, but later generations unfit or sterile.

- **Hybrid incompatibilities:** Dobzhansky–Muller interactions disrupt cellular/biochemical functions.

4.3 ROLE OF GENES AND GENOMES

- Divergence in key genes affecting mate recognition, pheromones and behavior.

- Divergence in developmental genes (e.g., Hox genes) leads to morphological differences.

- Genes in ecological adaptation (e.g., opsins for vision, detoxification genes) drive niche differentiation.

- Epigenetic changes can alter gene expression without changing DNA sequence.

4.4 GENOMIC ISLANDS OF DIVERGENCE

Regions of low recombination accumulate high divergence ("islands") while rest of genome remains similar.

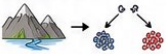
- Caused by inversions, chromosomal rearrangements or selection.

High divergence (island)

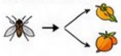
- Important in rapid speciation, especially in recently diverged species.

4.5 PATHWAYS TO SPECIATION (MOLECULAR PERSPECTIVE)

Allopatric speciation:
Geographic isolation → reduced gene flow → accumulation of molecular differences → RI.



Sympatric speciation:
Divergence within same area via disruptive selection, polyploidy, host shift, or behavioral isolation.



Parapatric speciation:
Divergence across environmental gradients with limited gene flow and selection.

Environment gradient

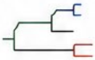
5. EXAMPLES

- Cichlid fishes in African rift lakes – rapid diversification via ecological and sexual selection.

- *Drosophila* – changes in courtship songs and pheromones lead to reproductive isolation.

6. MOLECULAR EVIDENCE FOR SPECIATION

- DNA barcoding and phylogenomic data reveal divergence and species boundaries.

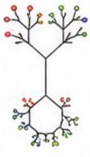


- Transcriptomics and proteomics show gene expression divergence.

- Whole genome comparisons identify genes and pathways under selection in diverging lineages.

7. SUMMARY

- ✓ Mutations, recombination and genomic changes generate variation.
- ✓ Isolation (geographic, ecological or behavioral) reduces gene flow.
- ✓ Divergence in genes, regulation and chromosomes leads to reproductive isolation.
- ✓ Over time, prezygotic and postzygotic barriers become complete, producing new species.

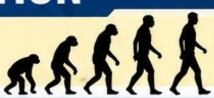


KEY TAKE-HOME MESSAGE

Speciation is fundamentally a genetic and molecular process—variation arises, divergence accumulates, and reproductive barriers evolve, ultimately producing distinct, independently evolving species.

RECENT TRENDS IN HUMAN EVOLUTION

Human evolution is a continuous process shaped by genetics, environment and culture.
Recent advances in science have given new insights into our origin, diversity and future.



KEY AREAS OF RECENT TRENDS

1. GENETIC AND MOLECULAR APPROACHES

DNA analysis, ancient DNA and genome sequencing reveal human origins, migrations and relationships.

2. FOSSIL DISCOVERIES AND RE-DATING

New fossils and advanced dating techniques refine the human evolution timeline.

3. ARCHAEOLOGICAL ADVANCES

New tools, symbolic behaviour, art and settlement patterns give insight into cultural evolution.

4. NEUROBIOLOGICAL AND COGNITIVE STUDIES

Study of brain evolution, cognition and behaviour explains what makes humans unique.

5. ENVIRONMENT, CLIMATE AND ADAPTATION

Climate change and environmental pressures shaped human adaptation, migration and survival.

6. HUMAN DIVERSITY AND POPULATION GENOMICS

Genetic studies show patterns of human variation, admixture and population history.

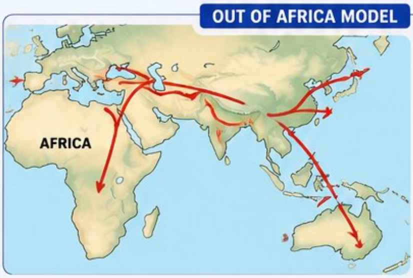
7. FUTURE PERSPECTIVES

Biotechnology, gene editing and AI may influence future human evolution.

1. GENETIC INSIGHTS – A MAJOR BREAKTHROUGH

- Mitochondrial DNA (mtDNA) studies show 'Out of Africa' origin (~60–70 kya).
- Y-chromosome and autosomal DNA reveal migration routes.
- Ancient DNA (aDNA) from Neanderthals, Denisovans and early modern humans shows interbreeding and gene flow.
- Genes related to immunity, skin colour, diet (lactase persistence), altitude adaptation evolved recently.

OUT OF AFRICA MODEL



KEY

→ Major migration routes

→ Time in thousand years ago

60–70 kya	Out of Africa
50–60 kya	West Eurasia
15–20 kya	East Asia
12–15 kya	Australia
10–15 kya	Americas

2. IMPORTANT FOSSIL DISCOVERIES (RECENT)

Sahelanthropus tchadensis
(~7 Mya)
One of the earliest hominins.

Homo naledi
(~300–200 kya)
Shows mixture of primitive and advanced traits.

Denisovans
(~40–50 kya)
Known from DNA and some bone fragments.

Jebel Irhoud
(Morocco)
(~300 kya)
Early *Homo sapiens* fossils.

Homo luzonensis
(Philippines)
(~67 kya)
New species of archaic human.

Advanced dating techniques: Radiometric dating, U-series, ESR, Paleomagnetism, Luminescence.

3. CULTURAL AND BEHAVIOURAL EVOLUTION

- Early stone tools → Acheulean, Mousterian, Microlithic industries.
- Symbolic behaviour: cave art, ornaments, burials.
- Language, social cooperation and culture drive human success.
- Agriculture (~12 kya) and domestication led to settled life and complex societies.

4. BRAIN AND COGNITIVE EVOLUTION

- Increase in brain size in *Homo* genus.
- Expansion of prefrontal cortex → planning, decision making, creativity.
- Evolution of speech, abstract thinking and problem solving.

5. HUMAN DIVERSITY – A CONTINUUM

- All modern humans belong to one species – *Homo sapiens*.
- Genetic variation is clinal (gradual) not racial.
- Admixture with archaic humans (Neanderthals ~1–4%, Denisovans in some Asian & Oceanian populations).
- Adaptations to local environments (e.g., high altitude, diet, climate, pathogens).

6. ENVIRONMENT & CLIMATE IMPACT

- Pleistocene climate fluctuations influenced migrations and adaptations.
- Humans adapted to cold, heat, altitude, diet changes and new pathogens.
- Environmental change continues to shape health, lifestyle and evolution.

EASY MNEMONIC

"GREAT HUMANS"

G – Genetics
R – Relics (Fossils)
E – Environment
A – Archaeology

T – Technology (Future)
H – Human Brain
U – Unity in Diversity
M – Migrations
A – Adaptations
N – New Discoveries
S – Social & Culture

7. FUTURE PERSPECTIVES

- Gene editing (CRISPR), synthetic biology may influence future evolution.
- Technology, AI and medicine can extend lifespan and enhance abilities.
- Ethical and social factors will decide the direction of human evolution.
- Evolution is not over – we are still evolving!

Genes → Environment → Culture & Society → Technology → Future Human

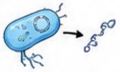
KEY TAKEAWAY Recent trends show that human evolution is shaped by genes, environment, culture and technology. It is a dynamic, ongoing process with a promising future.

7(b) CONSEQUENCES OF HORIZONTAL GENE TRANSFER IN BACTERIA

Horizontal Gene Transfer (HGT) is the movement of genetic material between organisms without being inherited from parent to offspring. It creates genetic variation and has many important consequences for bacteria and for us.

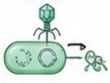
3 MAJOR MECHANISMS OF HGT

Transformation



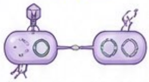
Uptake of free DNA from environment

Transduction



Transfer of DNA by bacteriophages

Conjugation

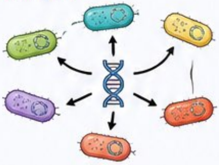


Transfer of plasmid or DNA directly between cells

MAJOR CONSEQUENCES OF HGT

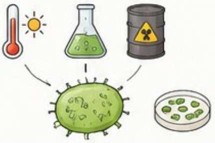
1 GENETIC DIVERSITY AND VARIATION

- Introduces new genes into bacterial populations.
- Increases genetic variability beyond mutation and natural selection.
- Provides raw material for evolution and adaptation.



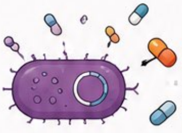
2 RAPID ADAPTATION TO ENVIRONMENT

- Bacteria can quickly acquire genes that help them survive in new or stressful environments.
- Helps in adaptation to extreme conditions (e.g., high temperature, salinity, toxins).



3 ANTIBIOTIC RESISTANCE

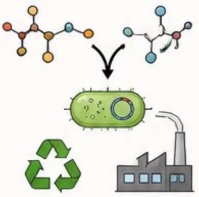
- One of the most significant consequences.
- Transfer of resistance genes (e.g., *bla, tet, sul, erm*) via plasmids, transposons, integrons.
- Leads to emergence of Multi-Drug Resistant (MDR), Extensively Drug Resistant (XDR) and Pan-Drug Resistant (PDR) strains.



HGT spreads resistance faster than clonal spread

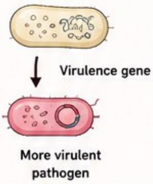
4 ACQUISITION OF NEW METABOLIC CAPABILITIES

- Bacteria gain genes for new metabolic pathways.
- Enables utilization of unusual or complex substrates.
- Important in biodegradation of pollutants and in industrial biotechnology.



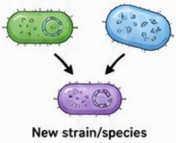
5 INCREASED VIRULENCE AND PATHOGENICITY

- Transfer of virulence genes (e.g., toxins, adhesins, secretion system genes) enhances pathogenic potential.
- Helps non-pathogenic strains become pathogenic.
- Contributes to emergence of new pathogenic clones.



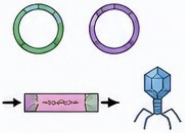
6 FORMATION OF NEW STRAINS AND SPECIES

- Exchange of large DNA segments can lead to new gene combinations.
- May result in emergence of new strains, biovars or even new species.
- Plays an important role in bacterial evolution and speciation.



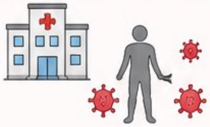
7 SPREAD OF MOBILE GENETIC ELEMENTS

- HGT mobilizes plasmids, transposons, integrons, genomic islands and prophages.
- These elements carry multiple beneficial genes.
- Leads to 'genetic hitchhiking' of genes.



8 IMPACT ON PUBLIC HEALTH

- Leads to outbreaks of resistant and highly virulent infections.
- Complicates treatment and infection control.
- Increases morbidity, mortality and healthcare cost.



9 BIOTECHNOLOGICAL AND ECOLOGICAL BENEFITS

- Used in genetic engineering and cloning.
- Helps in development of engineered strains for production of enzymes, antibiotics, vaccines.
- Important in microbial ecology and nutrient cycling.

KEY POINTS TO REMEMBER

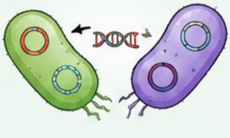
- HGT is a powerful force in bacterial evolution.
- It accelerates adaptation, survival and colonization.
- It can be beneficial (biotechnology, environment) or harmful (antibiotic resistance, virulence).
- Understanding HGT is essential for controlling infectious diseases and for using bacteria in a beneficial way.

EASY MNEMONIC "DARKVSPB"

D – Diversity
A – Adaptation
R – Resistance
K – New metabolic abilities
V – Virulence
S – New strains/species
P – Public health impact
B – Biotechnological benefits

IN A NUTSHELL

HGT makes bacteria smarter, stronger and more adaptable – both a challenge for medicine and an opportunity for science.



★ **EXAM TIP:** For 5 marks – write points with examples. For 10 marks – explain with mechanisms and significance.

Assignment Qus

DEBASISH
COLLECTION

ASSIGNMENT

Course Code: MZO-004
Assignment Code: MZO-004/TMA/2024
Maximum Marks: 100

Note: Attempt all questions. The mark for each question is indicated against it.

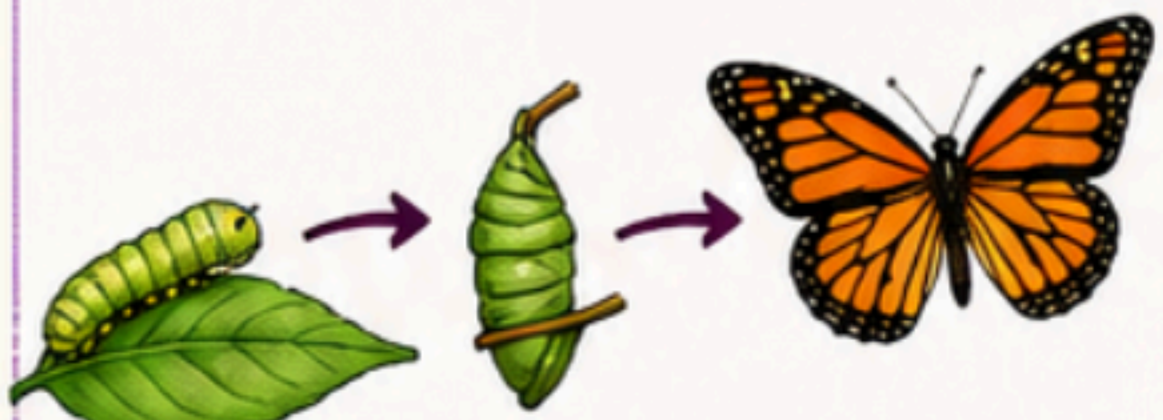
1. What is evolution? Describe the Charles Darwin's theory of evolution. (10)
2. Describe any two theories associated with the origin of life. (10)
3. Describe the concept of speciation in bacteria. (10)
4. What is molecular divergence? Describe the proteins that are studied as an example of Molecular clock. (4+6=10)
5. Describe the divergence of Bacteria and Archaea in terms of replication and translation systems. (10)
6. Describe any two agents of Horizontal gene transfer with the help of suitable diagrams. (10)
7. Compare the cellular and molecular characteristics of Bacteria, Archaea and Eukaryotes. (10)
8. Discuss the origin of multicellularity and evolution of bilateral symmetry in animals. (10)
9. Describe the consequences of genome and gene duplications. (10)
10. Define the following: (2½×4=10)
    a) Pseudogene
    b) Genetic drift
    c) Cladogenesis
    d) Biosystematics

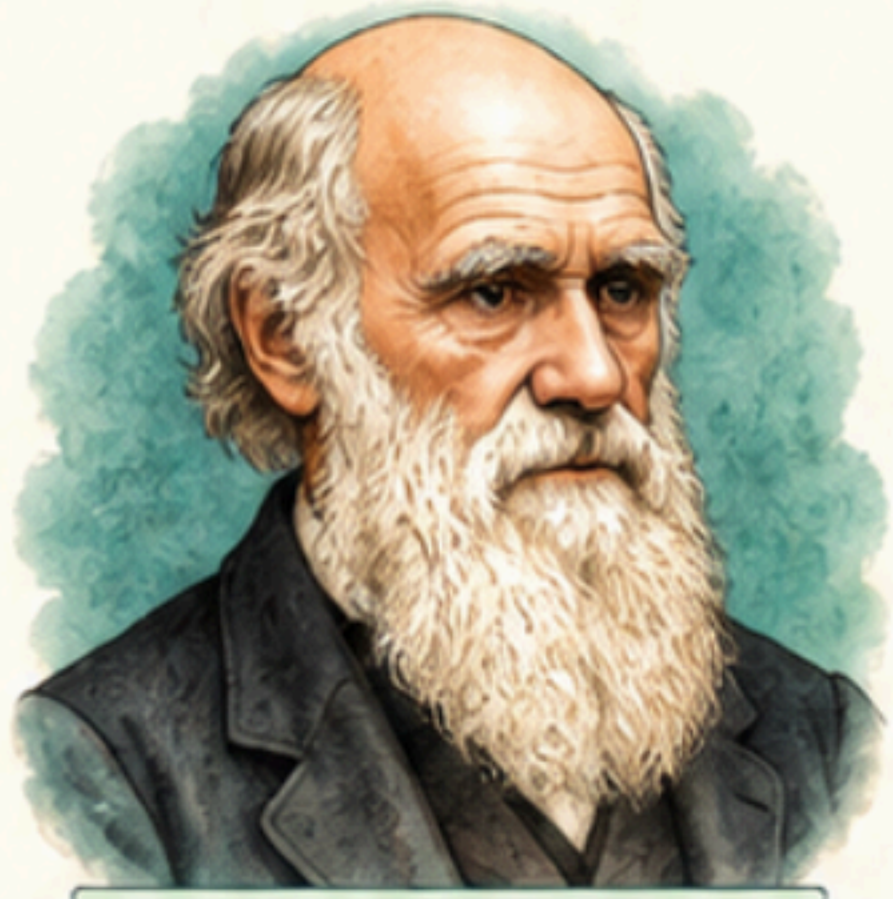
WHAT IS EVOLUTION?

CHARLES DARWIN'S THEORY OF EVOLUTION

1. WHAT IS EVOLUTION?

Evolution is the **gradual change** in the characteristics of living organisms (populations) over **many generations**. These changes help organisms to **survive** and **reproduce** in their environment. It explains the **diversity of life** on Earth.





CHARLES ROBERT DARWIN
(1809–1882)

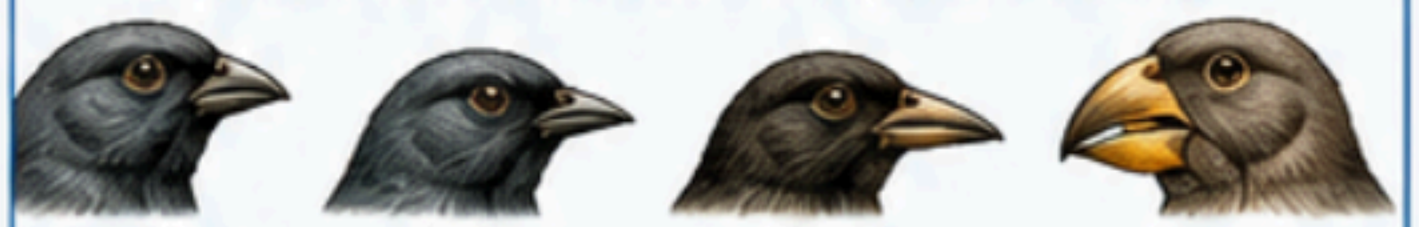
> "It is not the strongest of the species that survives, nor the most intelligent, but the one most responsive to change."

2. DARWIN'S OBSERVATIONS

During his voyage on **HMS Beagle** (1831–1836), Darwin observed:

- Organisms vary in size, shape, color, etc.
- Many more individuals are born than can survive.
- Species are well adapted to their environment.
- Similar species on different islands (e.g., Galápagos finches) had different beak shapes suited to different foods.

GALÁPAGOS FINCHES – DIFFERENT BEAKS

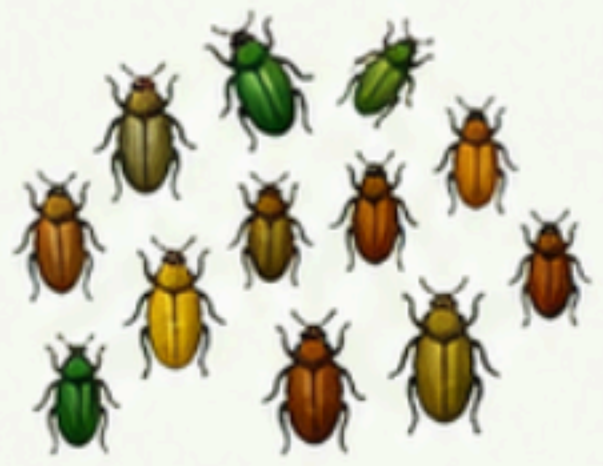


3. DARWIN'S THEORY OF EVOLUTION BY NATURAL SELECTION

Darwin proposed that evolution occurs through **NATURAL SELECTION**.

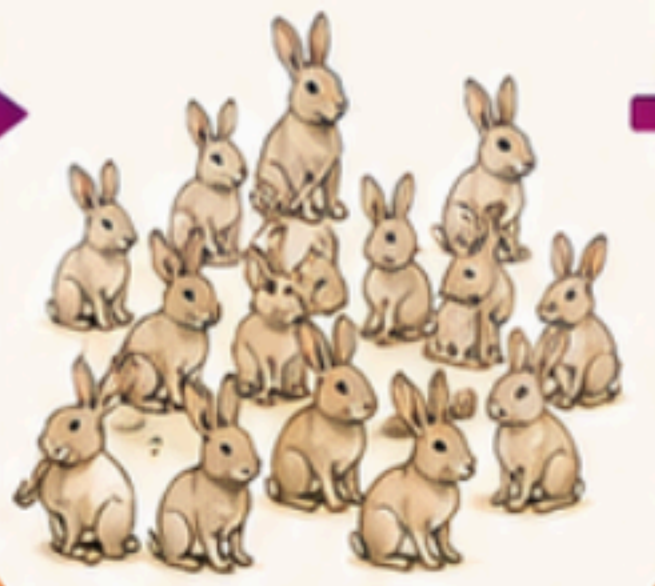
① VARIATION

Individuals in a population vary in many ways. (e.g., height, color, beak size)



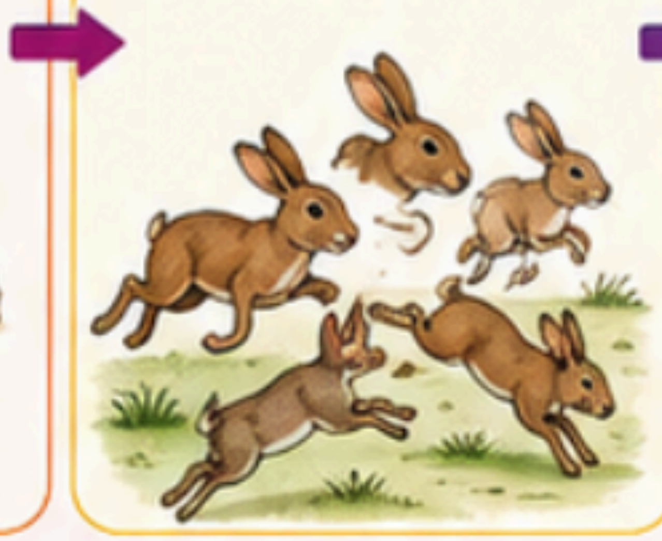
② OVERPRODUCTION

Organisms produce more offspring than can survive.



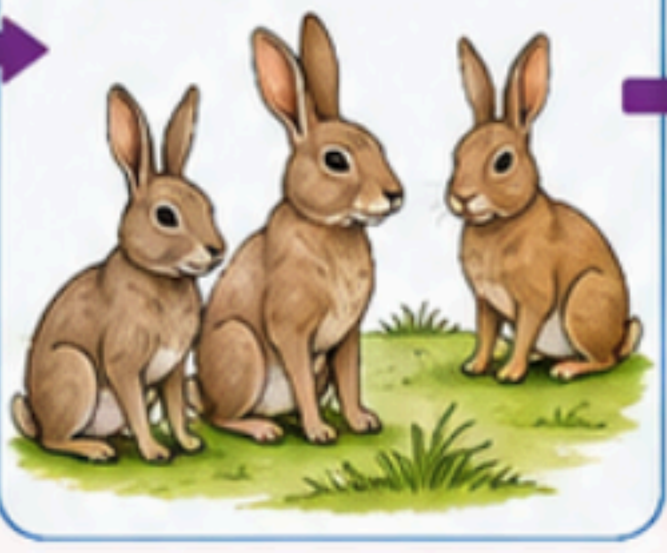
③ STRUGGLE FOR EXISTENCE

Limited resources like food, space, mates lead to competition.



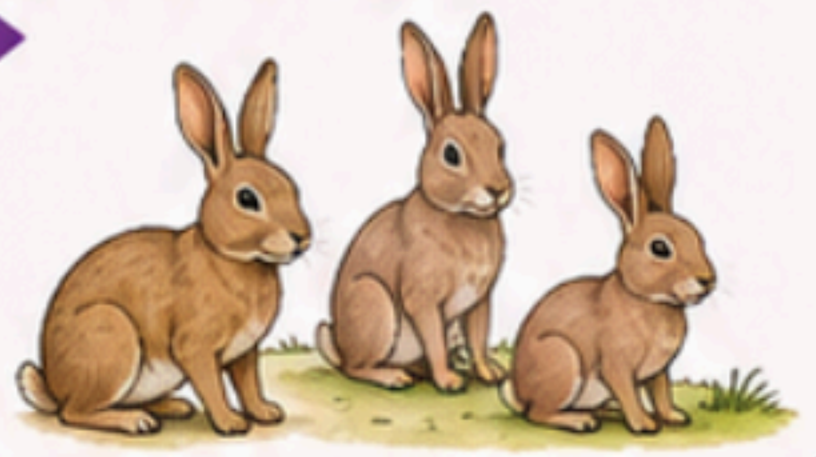
④ SURVIVAL OF THE FITTEST

Individuals with favorable variations survive and reproduce.



⑤ INHERITANCE & ACCUMULATION OF FAVOURABLE TRAITS

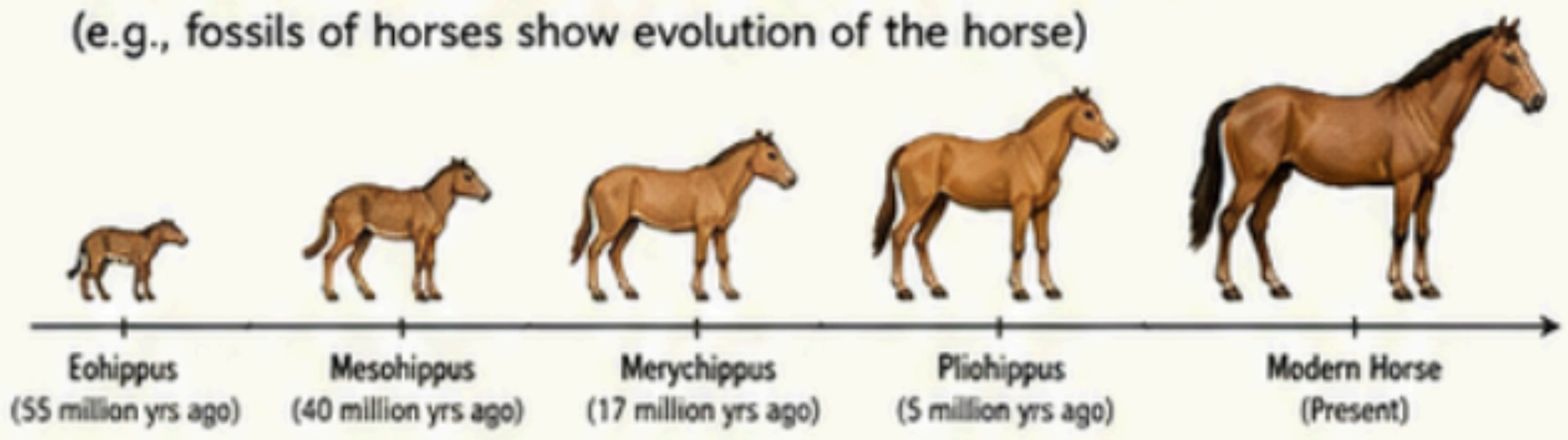
Favorable traits are passed on to offspring. Over many generations, these traits accumulate and the population changes.



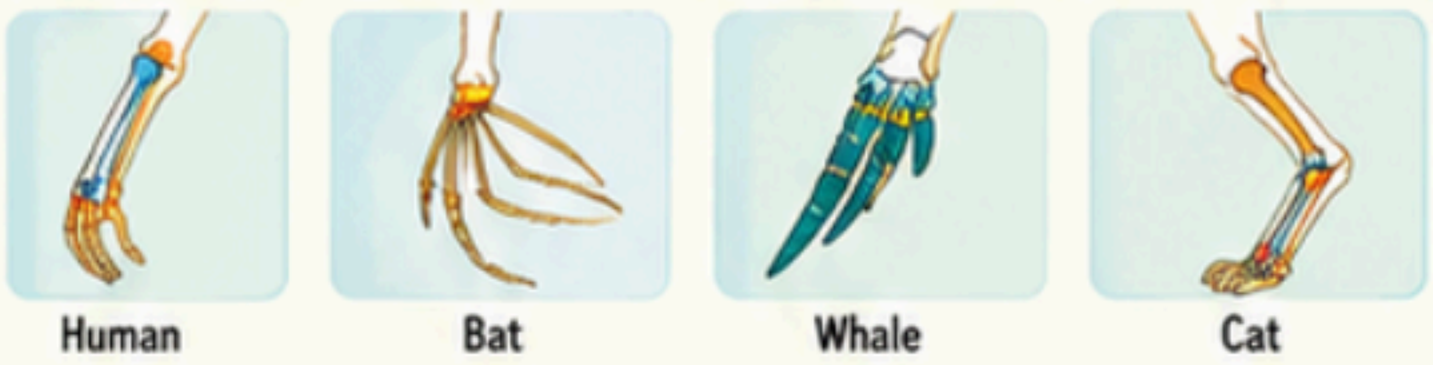
★ Over long periods of time, small changes accumulate and new species may arise. ★

4. EVIDENCE FOR EVOLUTION

- **Fossil record:** Shows gradual changes in organisms over time. (e.g., fossils of horses show evolution of the horse)



- **Comparative anatomy:** Similar structures in different organisms (e.g., forelimbs of human, bat, whale, cat) indicate common ancestry.



- **Embryological evidence:** Early embryos of different animals are similar.
- **Biogeography:** Similar species on the same islands/regions.
- **Molecular evidence:** Similarity in DNA and proteins among organisms.

5. SIGNIFICANCE OF DARWIN'S THEORY

- Explains the diversity of life and how species change over time.
- Helps us understand adaptation and survival in nature.
- Basis for many fields: genetics, conservation, medicine, agriculture, etc.
- Encourages scientific thinking and research.

KEY POINTS TO REMEMBER

- ★ Evolution is a natural process, not a goal-oriented one.
- ★ It occurs at the population level, not in individual lifetime.
- ★ Natural selection is the driving force of evolution.
- ★ All living organisms are related by common ancestry.

> "From so simple a beginning endless forms most beautiful and most wonderful have been, and are being, evolved." – Charles Darwin, "The Origin of Species" (1859)

ORIGIN OF LIFE ON EARTH

DESCRIBE ANY TWO THEORIES ASSOCIATED WITH THE ORIGIN OF LIFE

The origin of life refers to the appearance of the first living organisms on Earth from non-living matter through natural processes. Several theories have been proposed to explain this. Here are any two important theories:

1. CHEMICAL EVOLUTION THEORY (Oparin – Haldane Theory)

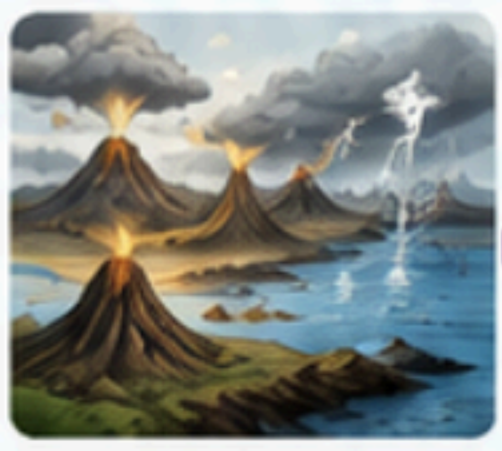
Overview

Proposed independently by **A. I. Oparin** (1924) and **J. B. S. Haldane** (1929).

It suggests that life arose gradually on Earth through a series of chemical reactions over millions of years.

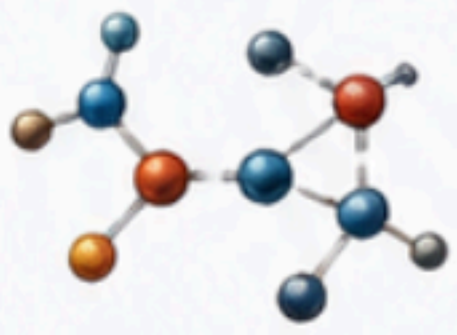
Key Steps / Explanation

1. Primordial Earth



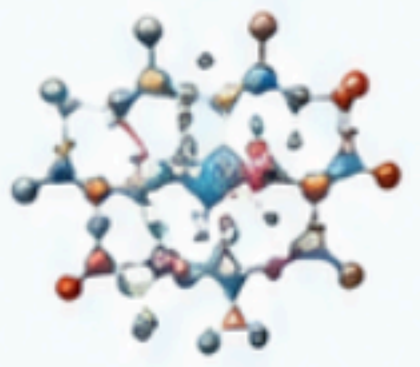
Early Earth (about 4.5 billion years ago) had a reducing atmosphere composed of gases like methane (CH_4), ammonia (NH_3), hydrogen (H_2), and water vapour (H_2O) but no oxygen.

2. Formation of Organic Molecules



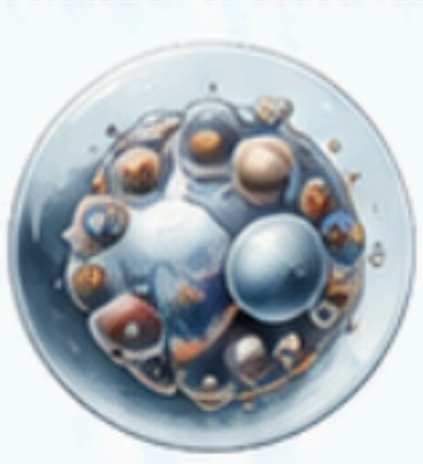
Energy sources such as lightning, UV radiation and volcanic heat caused chemical reactions that formed simple organic molecules like amino acids, sugars, and bases.

3. Formation of Complex Compounds



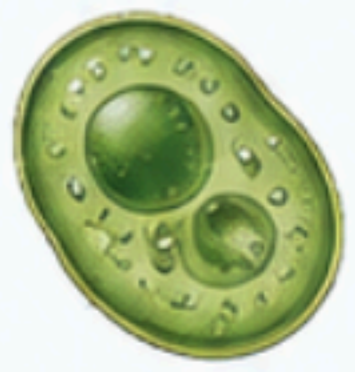
These simple molecules combined to form complex organic compounds such as proteins, nucleic acids and lipids.

4. Formation of Coacervates



Complex molecules aggregated to form tiny droplets called coacervates (microspheres) which had a membrane-like boundary and could trap other molecules.

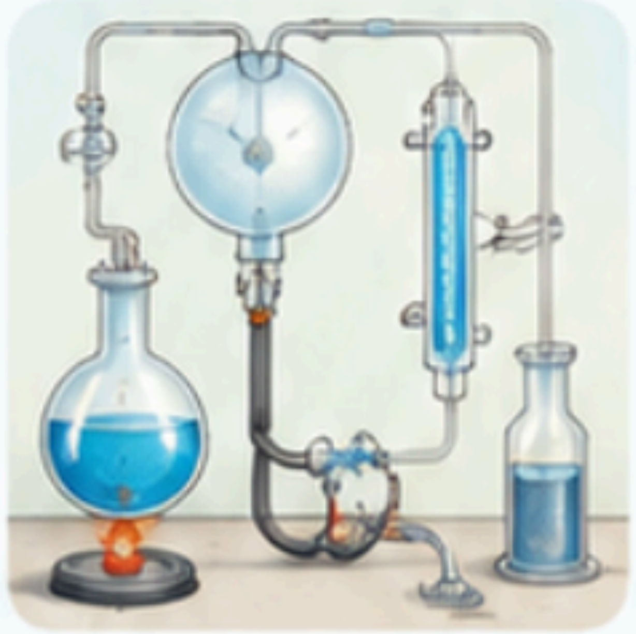
5. Origin of Life



Coacervates became more stable and developed self-replication and metabolism, leading to the first primitive living organisms.

Key Points

- Life arose from non-living matter through purely chemical processes.
- It was a gradual and step-by-step process.
- The first life forms were simple, anaerobic and heterotrophic.
- Supported by the Miller–Urey experiment (1953): amino acids were produced in the lab by simulating early Earth conditions.



Evaluation / Significance

- ✓ Explains the chemical origin of life scientifically.
- ✓ Supported by experimental evidence.
- ✓ However, exact conditions of early Earth are still uncertain.
- ✓ Does not explain how the first self-replicating molecule (like RNA) originated.

2. PANSPERMIA THEORY

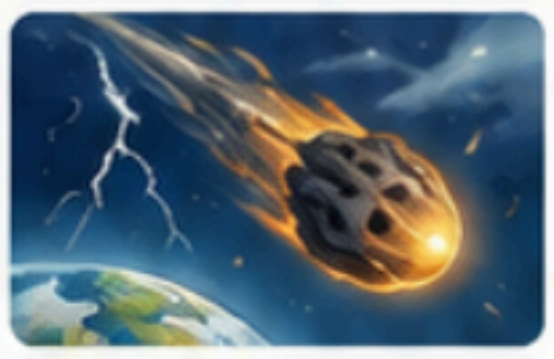
Overview

Proposed by **Svante Arrhenius** (1903) and later supported by **Fred Hoyle** and **Chandra Wickramasinghe**.

It suggests that life did not originate on Earth but was brought here from space by cosmic bodies.

Explanation / Types

1. Lithopanspermia

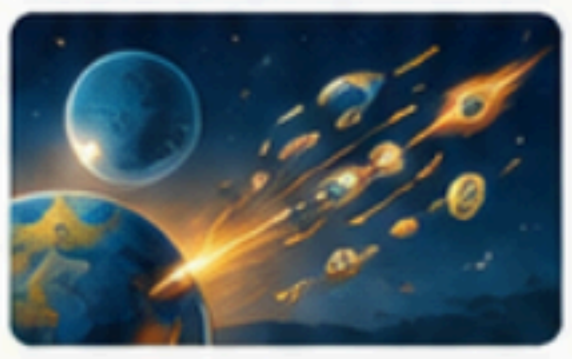


Microbes or spores were carried on meteorites or comets and fell on Earth.

2. Directed Panspermia

Advanced civilizations from other planets intentionally seeded life on Earth.

3. Radiopanspermia



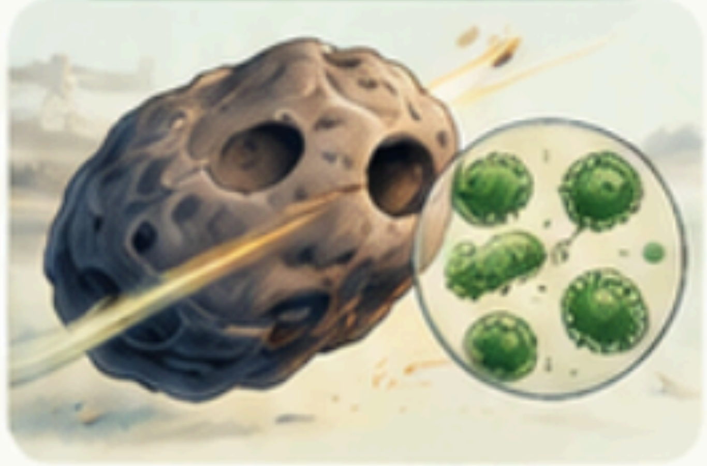
Life exists as microscopic spores or cells that travel through space carried by radiation pressure.

Key Points

- Earth is a suitable place for life to exist.
- Microorganisms can survive in harsh conditions of space (supported by experiments on bacterial spores).
- Explains the sudden appearance of life without intermediate stages on Earth.

Supporting Evidence

- Organic molecules have been found in meteorites.
- Some microbes (e.g., *Deinococcus*) can survive in extreme conditions of radiation and vacuum.
- Comets and meteorites may have carried water and organic compounds.



Limitations

- ✗ No direct evidence of living organisms in space yet.
- ✗ It does not explain the origin of life, only its transfer.
- ✗ Survival of organisms during long space travel is uncertain.
- ✗ Highly dependent on chance.

COMPARISON TABLE

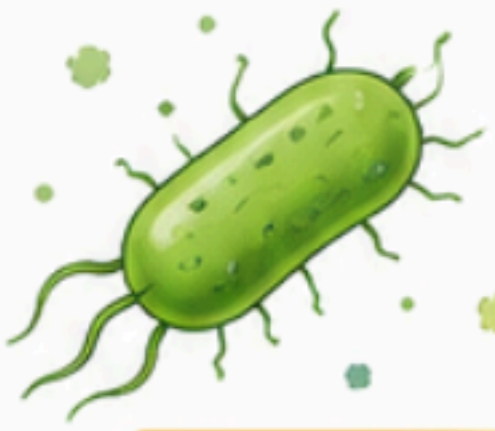
Feature	Chemical Evolution Theory	Panspermia Theory
Origin of life	Life arose on Earth from non-living matter.	Life came from outer space.
Proposed by	Oparin and Haldane	Svante Arrhenius, Fred Hoyle, Chandra Wickramasinghe
Main idea	Step-by-step chemical evolution on early Earth.	Transfer of life (spores/microbes) from space to Earth.
Evidence	Miller–Urey experiment, formation of organic compounds.	Meteorites with organics, survival of microbes in space.
Limitation	Does not explain first self-replicating molecule.	No direct proof of life in space.

CONCLUSION

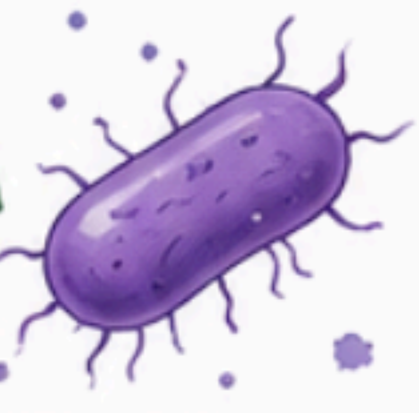
Both theories attempt to answer the greatest question of biology – "How did life begin?" The **Chemical Evolution Theory** explains the natural development of life on Earth, while the **Panspermia Theory** suggests that life may have **come from elsewhere. More research and discoveries are** needed to fully understand the origin of life.

Think! Could life exist elsewhere in the universe? The search continues...!

The study of the origin of life helps us understand our past, our place in the universe, and the possibility of life beyond Earth.



SPECIATION IN BACTERIA

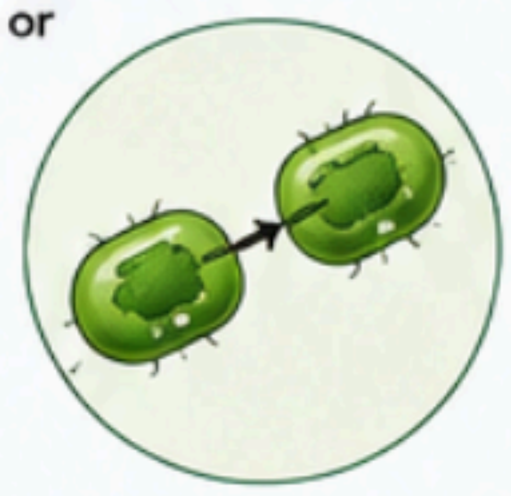


• How new bacterial species arise •

Speciation is the process by which new and distinct species evolve from pre-existing ones.
In bacteria, speciation occurs when populations become **genetically distinct**
and **reproductively isolated** from each other.

1. WHAT IS SPECIATION IN BACTERIA?

Bacteria reproduce **asexually** by binary fission and exchange genes by **horizontal gene transfer (HGT)**. Speciation in bacteria occurs when a population or lineage becomes sufficiently different from its ancestral population that it can **no longer interbreed** (genetically exchange) effectively with it.



Key Point

In bacteria, reproductive isolation is not complete like in higher organisms, but genetic discontinuity and ecological separation lead to divergence and new species formation.

2. HOW SPECIATION OCCURS IN BACTERIA

Bacterial speciation is mainly driven by:

- **Genetic Variation** – mutations, gene duplications, insertions, deletions, recombination.
- **Horizontal Gene Transfer (HGT)** – transformation, transduction, conjugation introduce new genes.
- **Natural Selection** – environmental pressures select beneficial variations.
- **Genetic Drift** – random changes in small populations.
- **Geographic or Ecological Isolation** – limits gene flow between populations.

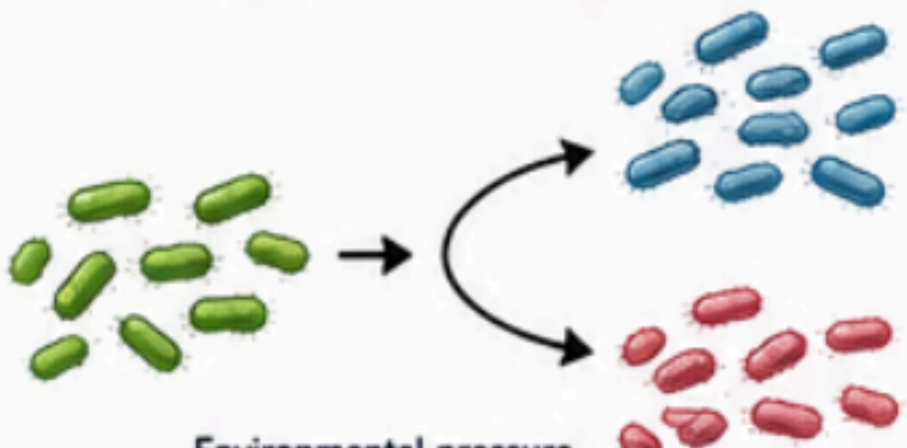
Key Point

The accumulation of differences leads to **genetic divergence** and eventually new species.

3. MECHANISMS AND PATHWAYS OF SPECIATION IN BACTERIA

A. Mutation and Natural Selection

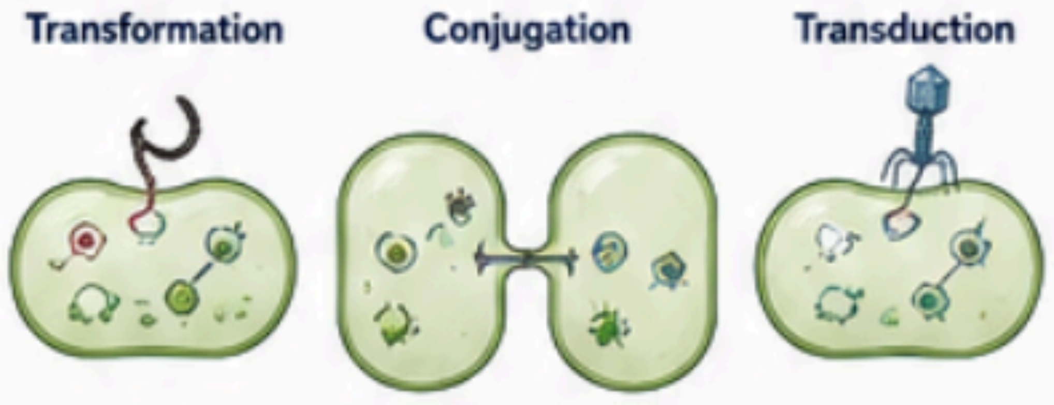
Random mutations create variation. Under different environments, natural selection favors beneficial mutations. Over time, populations diverge.



Environmental pressure leads to divergence

B. Horizontal Gene Transfer (HGT)

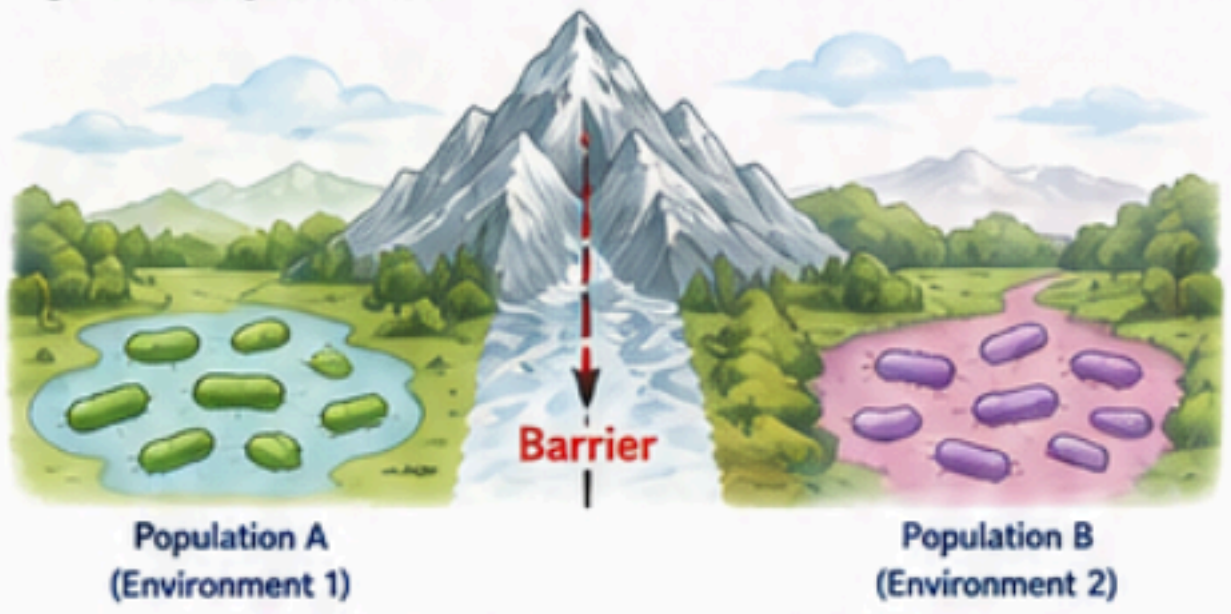
Acquisition of new genes through transformation, conjugation or transduction provides new functions (e.g., antibiotic resistance, metabolic capabilities) leading to ecological specialization.



HGT introduces new traits → adaptive radiation

C. Geographic / Ecological Isolation

Physical barriers or different niches limit gene flow. Populations adapt to local conditions and become genetically distinct.

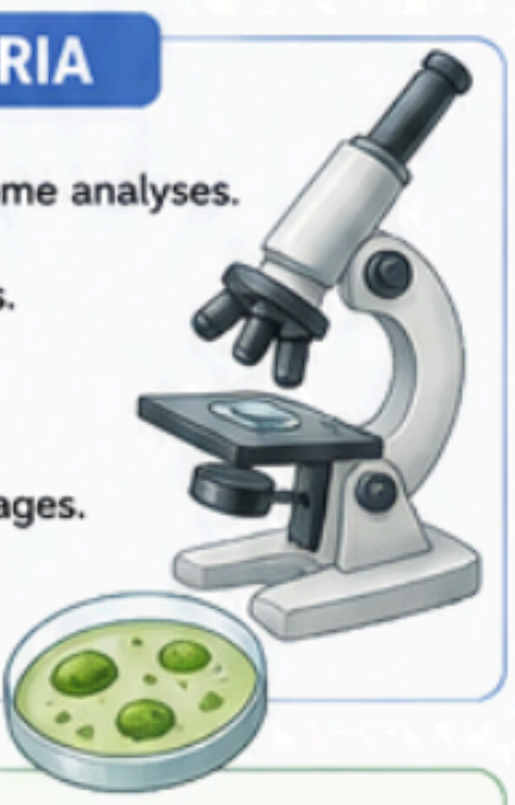


Isolation → divergence → new species

4. EXAMPLES OF BACTERIAL SPECIATION

E. coli Lineages		Different strains of *E. coli* have evolved from a common ancestor but adapted to different hosts (human, animals, environment) and show genetic distinctness.
Pathogenic Bacteria		*Yersinia pestis* (plague), *Vibrio cholerae* (cholera) and *Vibrio parahaemolyticus* evolved from close relatives through gene gain and niche adaptation.
Antibiotic Resistance		Bacterial populations exposed to antibiotics evolve into new resistant lineages with distinct genomes and phenotypes.

5. EVIDENCE FOR SPECIATION IN BACTERIA



- ✓ Genetic divergence in 16S rRNA sequences and whole-genome analyses.
- ✓ Differences in biochemical, physiological and metabolic traits.
- ✓ Distinct ecological niches and host specificities.
- ✓ Inability to exchange genes efficiently between diverged lineages.
- ✓ Recognized by modern taxonomy as separate species.

6. STEPS IN THE PROCESS OF SPECIATION (SUMMARY FLOW)

1 Ancestral Population
A single bacterial population occupies a habitat.

→

2 Variation Arises
Mutations, gene duplications and HGT create genetic diversity.

→

3 Isolation
Geographic or ecological barriers reduce or stop gene flow.

→

4 Divergence
Different environments select different traits; populations diverge genetically.

→

5 New Species Formed
Populations become distinct and are considered new bacterial species.

7. IMPORTANCE

- Helps bacteria adapt to new environments and hosts.
- Leads to emergence of useful strains (e.g., probiotics, industrial microbes).
- Also leads to harmful strains (e.g., pathogens, antibiotic resistant bacteria).
- Understanding speciation helps in disease control, antibiotic development and biotechnology.

8. KEY TAKEAWAY

Speciation in bacteria is a gradual process of **genetic divergence** driven by **mutation**, **horizontal gene transfer**, **natural selection**, **genetic drift and isolation**. Over time, populations become distinct in their genetic makeup, ecological adaptations and phenotypes, resulting in new bacterial species.

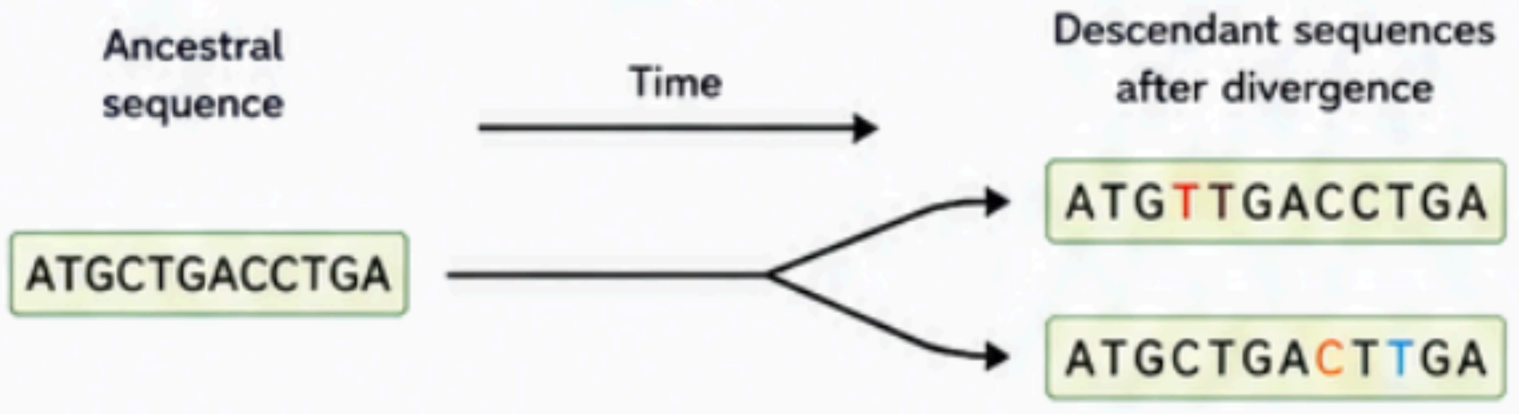
Tiny organisms, big evolution — bacteria continue to diversify and shape life on Earth!

WHAT IS MOLECULAR DIVERGENCE?
AND THE PROTEINS USED IN MOLECULAR CLOCK

Molecular divergence is the process by which DNA, RNA or protein sequences accumulate differences between populations or species over time due to **mutations** and natural selection. These differences can be used to estimate the time of divergence of lineages using the concept of a **molecular clock**.

1. WHAT IS MOLECULAR DIVERGENCE?

- It refers to the accumulation of heritable genetic or protein sequence differences between taxa.
- Differences arise mainly due to **point mutations**, insertions, deletions, gene duplications and selection.
- The more time has passed since two lineages diverged, the greater the molecular differences.
- These differences are measured at the molecular level and used to infer evolutionary relationships.



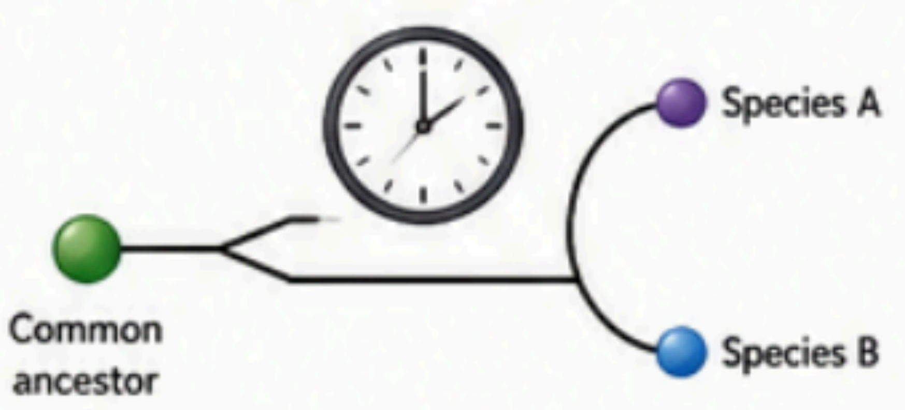
Key Point

Greater molecular divergence → Greater evolutionary distance
Fewer differences → More recent divergence

2. MOLECULAR CLOCK: AN OVERVIEW

- The molecular clock hypothesis states that molecular changes (accumulation of mutations) occur at a relatively constant rate over time.
- By measuring the amount of molecular divergence, we can estimate the time since two species diverged from a common ancestor.
- The rate may vary among genes and lineages, but some molecules evolve at a nearly constant rate and are useful as "molecular clocks".

Molecular clock concept



Formula

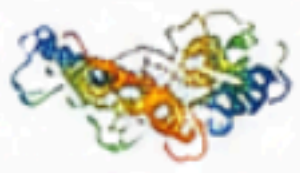
$$\text{Time of divergence (T)} = \frac{\text{Molecular divergence (D)}}{2 \times \text{Rate of evolution (r)}}$$

(The factor 2 accounts for changes in both lineages)

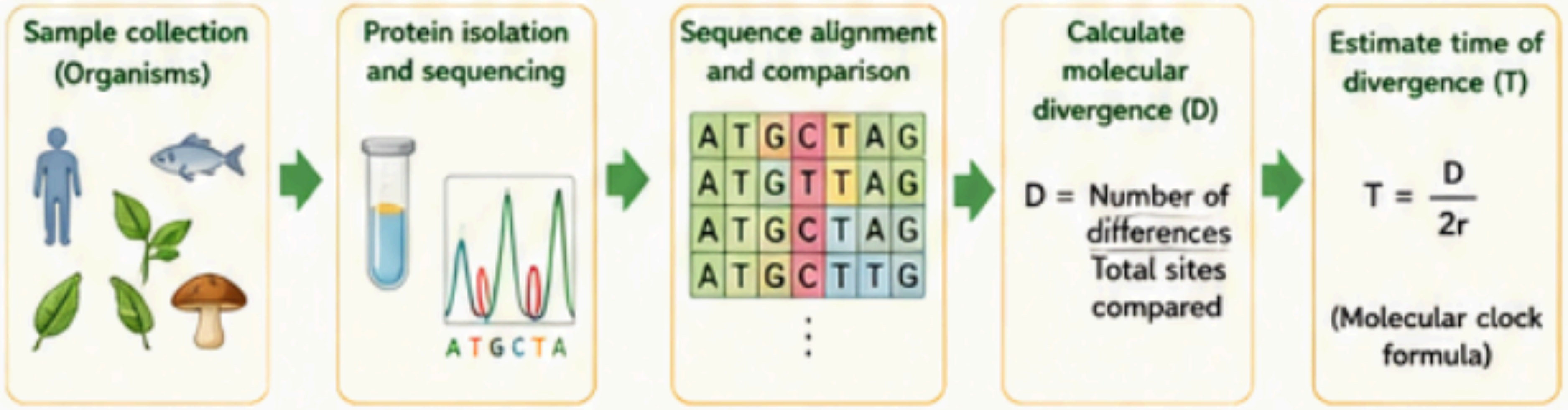
3. PROTEINS USED AS MOLECULAR CLOCKS (EXAMPLES)

Proteins used in molecular clock studies are generally those that are:

✓ Present in all organisms ✓ Functionally important ✓ Evolve slowly and steadily ✓ Have conserved regions for alignment

Protein	Also called / Found in	Why it is used	Features	Rate of Evolution	Applications (Examples)
Cytochrome c (Cyt c)	Heme-containing protein in mitochondria of all aerobic organisms (plants, animals, fungi, many bacteria)	Highly conserved function in electron transport chain; small size, easy to sequence.	~104 amino acids; very few changes over long evolutionary periods; presence of both conserved and variable regions.	★★☆☆☆ Slow (ideal for deep evolutionary studies)	Used to estimate divergence of vertebrates, insects, plants, fungi, and even bacteria; helped establish the molecular clock concept (Zuckerkandl & Pauling, 1962).
Hemoglobin (α and β chains)	Oxygen-transport protein in red blood cells of vertebrates and some invertebrates	Essential function; moderate conservation; both conserved and variable regions present.	~141 (α) and ~146 (β) amino acids per chain; changes more than Cyt c but still useful.	★★★☆☆ Moderate (used for intermediate divergence)	Used in studying primates, rodents, birds and other vertebrates; helps in understanding evolutionary relationships at genus/family levels.
Serum albumin (Albumin) 	Abundant plasma protein in vertebrates	Abundant, easy to isolate; good for studying more recent divergence.	~585 amino acids; more variable than Cyt c and hemoglobin.	★★★★☆ Relatively fast (used for recent evolutionary events)	Used for studying closely related species and population-level divergence.
Ribosomal proteins (L7/L12)	Found in ribosomes of all living organisms	Universal, essential for ribosome structure and function.	Small proteins (L7 ~ ~100 aa); contain both conserved and variable regions.	★☆☆☆☆ Very slow (suitable for deepest phylogeny)	Used for ancient divergence studies across major domains (e.g., bacteria vs. eukaryotes).

4. HOW PROTEINS ARE USED IN MOLECULAR CLOCK STUDIES



Sample collection (Organisms) → Protein isolation and sequencing → Sequence alignment and comparison → Calculate molecular divergence (D) → Estimate time of divergence (T)

$$D = \frac{\text{Number of differences}}{\text{Total sites compared}}$$

$$T = \frac{D}{2r}$$

(Molecular clock formula)

5. ASSUMPTIONS AND LIMITATIONS

Assumptions

- Mutations accumulate at a roughly constant rate.
- The compared sequences are homologous.
- Natural selection does not strongly affect the rate.

Limitations

- Mutation rates vary among lineages and environments.
- Some proteins evolve under selection pressure.
- Saturation: multiple mutations at same site may hide true divergence.
- Calibration (fossil record) is needed for absolute time estimates.

6. IMPORTANCE OF MOLECULAR DIVERGENCE AND MOLECULAR CLOCK

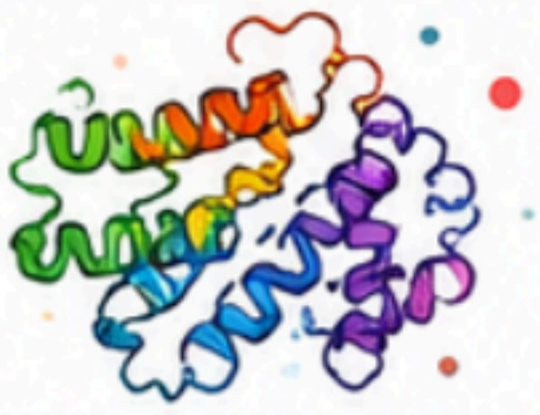
- ✓ Helps in reconstructing evolutionary relationships and phylogenetic trees.
- ✓ Estimates time of divergence of species and major evolutionary events.
- ✓ Correlates molecular data with fossil record → molecular phylogeny + paleontology.
- ✓ Useful in taxonomy, conservation biology, and evolutionary studies.
- ✓ Explains evolutionary patterns in both recent and ancient lineages.

KEY TAKEAWAY

Molecular divergence is the accumulation of molecular differences over time between species. By studying proteins like Cytochrome c, Hemoglobin, Serum albumin and Ribosomal proteins, scientists use the molecular clock to estimate evolutionary distances and divergence times, helping us understand the history of life on Earth.

From molecules to timelines — molecular divergence and the molecular clock reveal the story of evolution.

WHAT IS MOLECULAR DIVERGENCE?

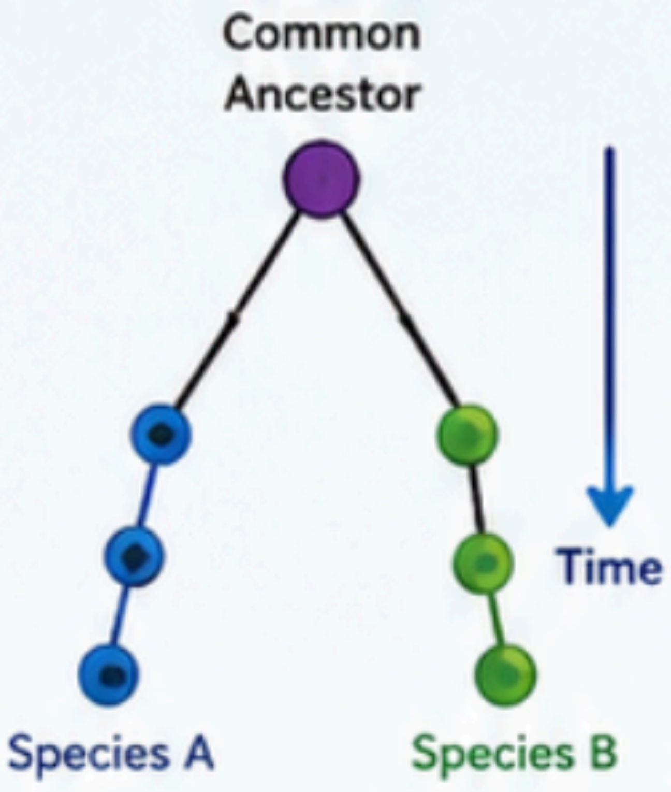


And the Proteins Studied as an Example of Molecular Clock

1 WHAT IS MOLECULAR DIVERGENCE?

- **Molecular divergence** is the process by which DNA, RNA or protein sequences accumulate heritable changes (mutations) over time, causing species or genes to become different from their common ancestors.
- These changes act as a molecular record of evolutionary time.
- The greater the number of differences in molecular sequences between two species, the longer ago they diverged from a common ancestor.
- **Basis of Molecular Clock Hypothesis:** If mutations accumulate at a fairly constant rate, molecular differences can be used to estimate the time of divergence.

DIVERGENCE OVER TIME



Mutations accumulate independently in each lineage → sequences diverge.

2 MOLECULAR CLOCK HYPOTHESIS

Proposed by **Zuckerkandl and Pauling** (1962).

- States that most genes and proteins evolve at a relatively constant rate.
- Therefore, the number of molecular differences is directly proportional to the time since divergence.
- It allows scientists to estimate evolutionary timelines even in the absence of fossils.

FORMULA (Simplified)

Time since divergence (T) = $\frac{K}{2r}$

Where,

K = number of differences per site between two sequences

r = rate of change (substitutions per site per million years)

2 = because changes accumulate independently in both lineages

3 PROTEINS STUDIED AS EXAMPLES OF MOLECULAR CLOCK

Several proteins have been extensively used to test molecular clock hypothesis.

1. CYTOCHROME c

- Small heme protein (~104 amino acids) located in the mitochondrial electron transport chain.
- Present in nearly all aerobic organisms.
- Functions: Carries electrons from cytochrome b to cytochrome oxidase.

Why used as molecular clock?

- Ubiquitous and essential → strong functional constraint.
- Evolves slowly and at a fairly constant rate.
- Amino acid sequence comparisons among mammals, birds, fish, plants, and yeast show a linear relationship between sequence divergence and evolutionary time.

Example of Divergence

Human vs Chimpanzee: 1 aa difference (very recent divergence)

Human vs Yeast: ~40 aa differences (ancient divergence)

2. HEMOGLOBIN

- Oxygen transport protein in red blood cells.
- Tetramer of two α and two β globin chains.
- Widely conserved in vertebrates.

Why used as molecular clock?

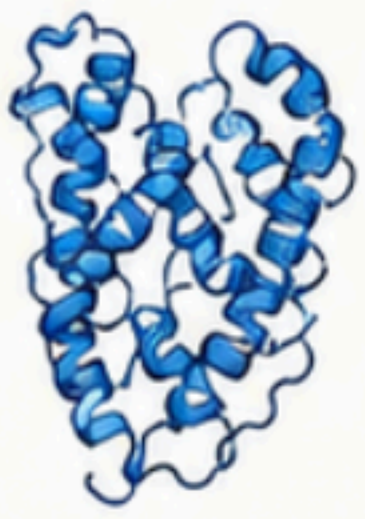
- Globin chains (α, β) are well characterized.
- Amino acid sequences show gradual changes among species.
- Rate of change is moderate and relatively constant within lineages.

Example of Divergence

Human vs Horse (β-chain): ~25 amino acid differences

Human vs Fish: ~50+ differences

3. SERUM ALBUMIN



- Major plasma protein; maintains osmotic pressure and transports various molecules.
- Very abundant and easy to purify.

Why used as molecular clock?

- Single-chain protein (~585 aa in humans).
- Evolves at an intermediate rate.
- Sequence comparisons provide estimates of divergence among vertebrates.

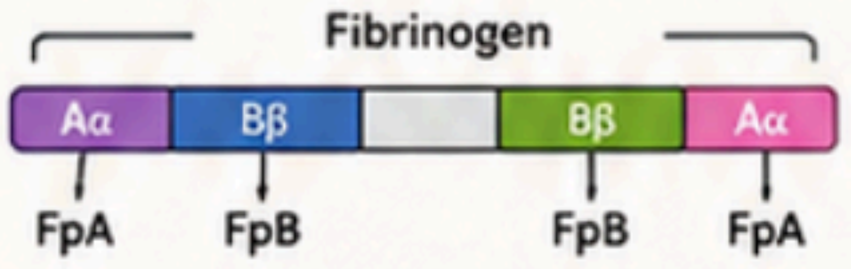
Example of Divergence

Human vs Cow: ~45 differences

Human vs Chicken: ~80 differences

Human vs Fish: ~120+ differences

4. FIBRINOPEPTIDES (FIBRINOGEN)



- Short peptide segments cleaved from fibrinogen during clot formation.
- Present in all vertebrates.
- These peptides accumulate sequence changes steadily.

Why used as molecular clock?

- Short size → easy sequencing.
- Evolve at a relatively constant rate.
- Useful for estimating divergence among vertebrate species.

Example of Divergence

Human vs Rabbit (FpB): ~10 differences

Human vs Shark: ~25+ differences

4 SIGNIFICANCE OF MOLECULAR CLOCK

- Helps estimate time of divergence between species.
- Supports construction of evolutionary trees (phylogenies).
- Useful when fossil record is incomplete or absent.
- Widely applied in evolutionary biology, conservation and taxonomy.

5 LIMITATIONS

- Mutation rates are not strictly constant in all lineages.
- Natural selection can alter rates of evolution.
- Different genes/proteins evolve at different rates.
- Saturation of changes at very long evolutionary times.

SUMMARY TABLE

Protein	Size (approx.)	Rate of Evolution	Why Suitable as Molecular Clock
Cytochrome c	~104 aa	Slow	Ubiquitous, essential, strong functional constraint
Hemoglobin (globin chains)	~140 aa (per chain)	Moderate	Well characterized, linear divergence
Serum Albumin	~585 aa	Intermediate	Abundant, single chain, moderate rate
Fibrinopeptides	Short (5–16 aa)	Relatively constant	Short, easy to sequence, steady changes

Conclusion: Molecular divergence provides a molecular record of evolution. Proteins such as cytochrome c, hemoglobin, serum albumin and fibrinopeptides have been powerful tools in applying the molecular clock to understand evolutionary time.

DESCRIBE ANY TWO AGENTS OF HORIZONTAL GENE TRANSFER

Horizontal gene transfer (HGT) is the movement of genetic material between organisms other than by vertical transmission (parent to offspring). It plays a major role in genetic diversity, evolution, antibiotic resistance and pathogenicity in microorganisms.

TWO MAJOR AGENTS OF HORIZONTAL GENE TRANSFER

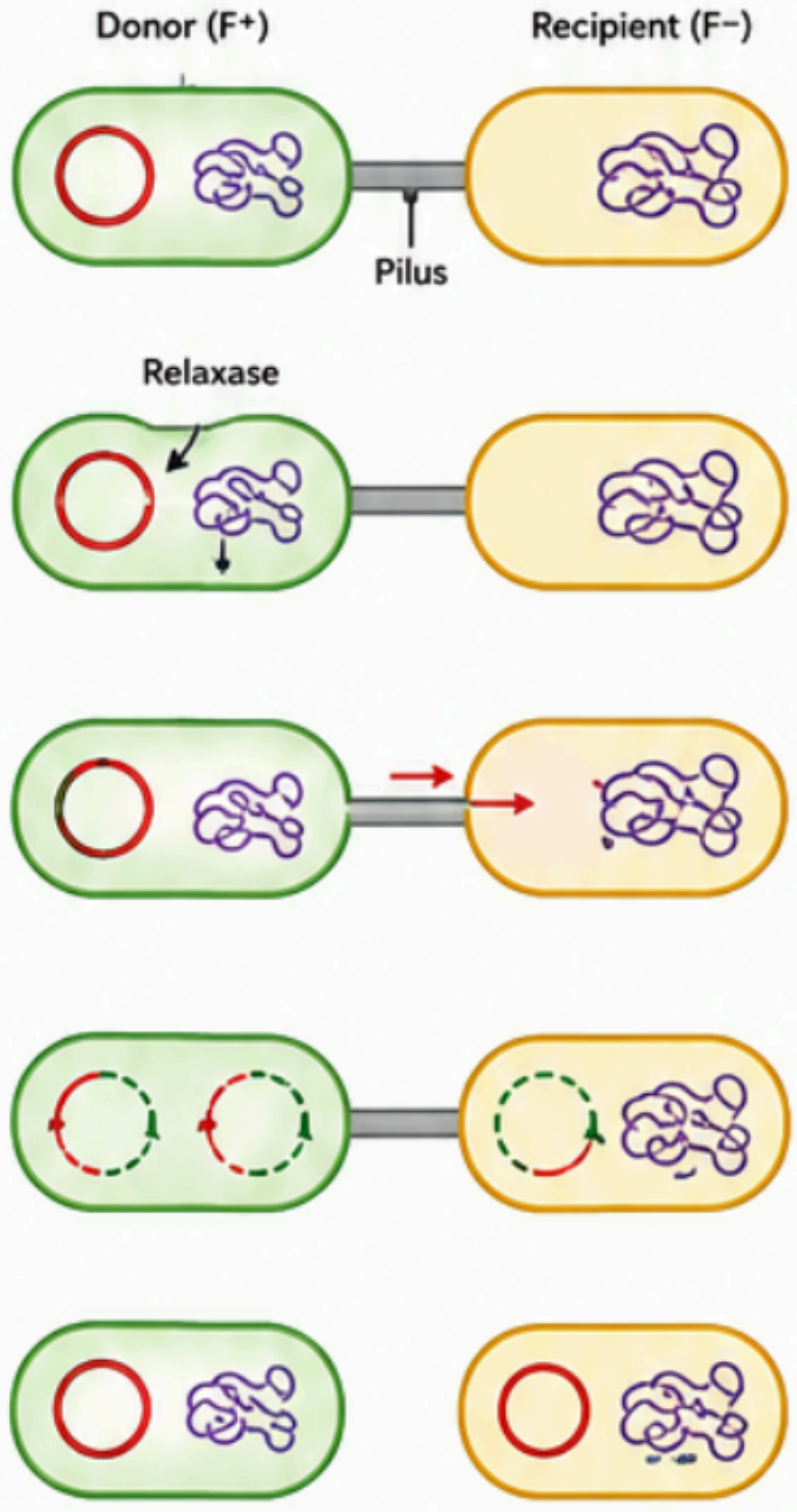
1 CONJUGATION

Conjugation is the direct transfer of DNA (usually plasmid) from a donor bacterium to a recipient bacterium through cell-to-cell contact.

KEY FEATURES

- Mediated by conjugative plasmids (e.g., F plasmid).
- Requires direct contact via a pilus (sex pilus).
- DNA is transferred as single-stranded DNA (ssDNA).
- Both plasmid (extra-chromosomal) and chromosomal DNA can be transferred.
- Recipient cell does not need to be genetically related.

MECHANISM (F+ DONOR → F− RECIPIENT)

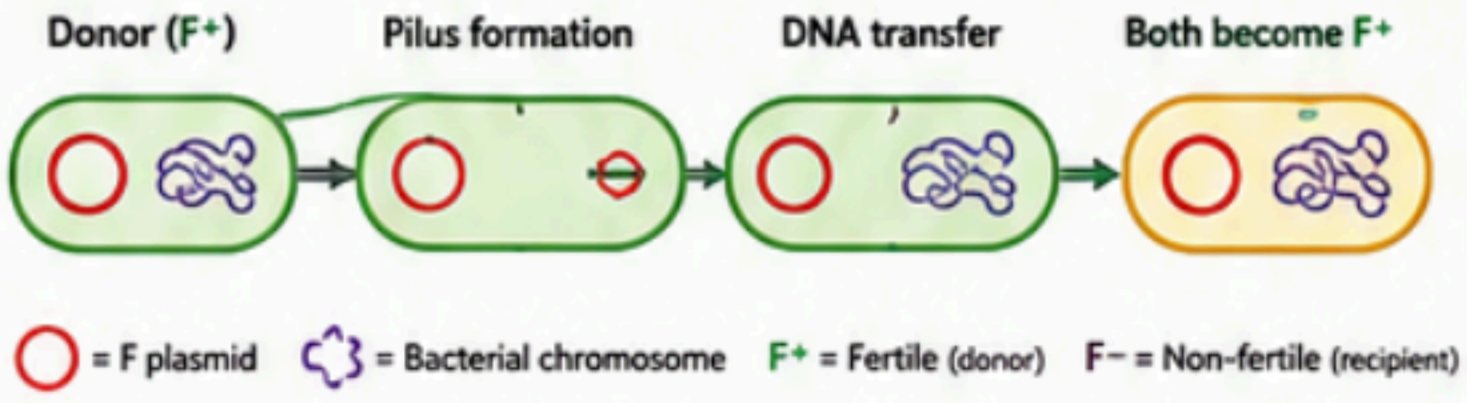


1. Donor (F+) cell with F plasmid forms a pilus with F− recipient cell.
2. Relaxase enzyme makes a nick (*oriT*) on the plasmid.
3. The ssDNA strand is transferred through the conjugation bridge to the recipient.
4. Both donor and recipient synthesize the complementary strand.
5. Both cells now contain a complete F plasmid and can act as donors.

SIGNIFICANCE

- ✓ Spreads antibiotic resistance (R plasmids), toxin production genes, degradative enzymes, and virulence factors.
- ✓ Important in evolution and adaptation of bacteria.
- ✓ Example: Transfer of R plasmids carrying β-lactamase gene between bacteria.

EXAMPLE DIAGRAM (SUMMARY)



2 TRANSDUCTION

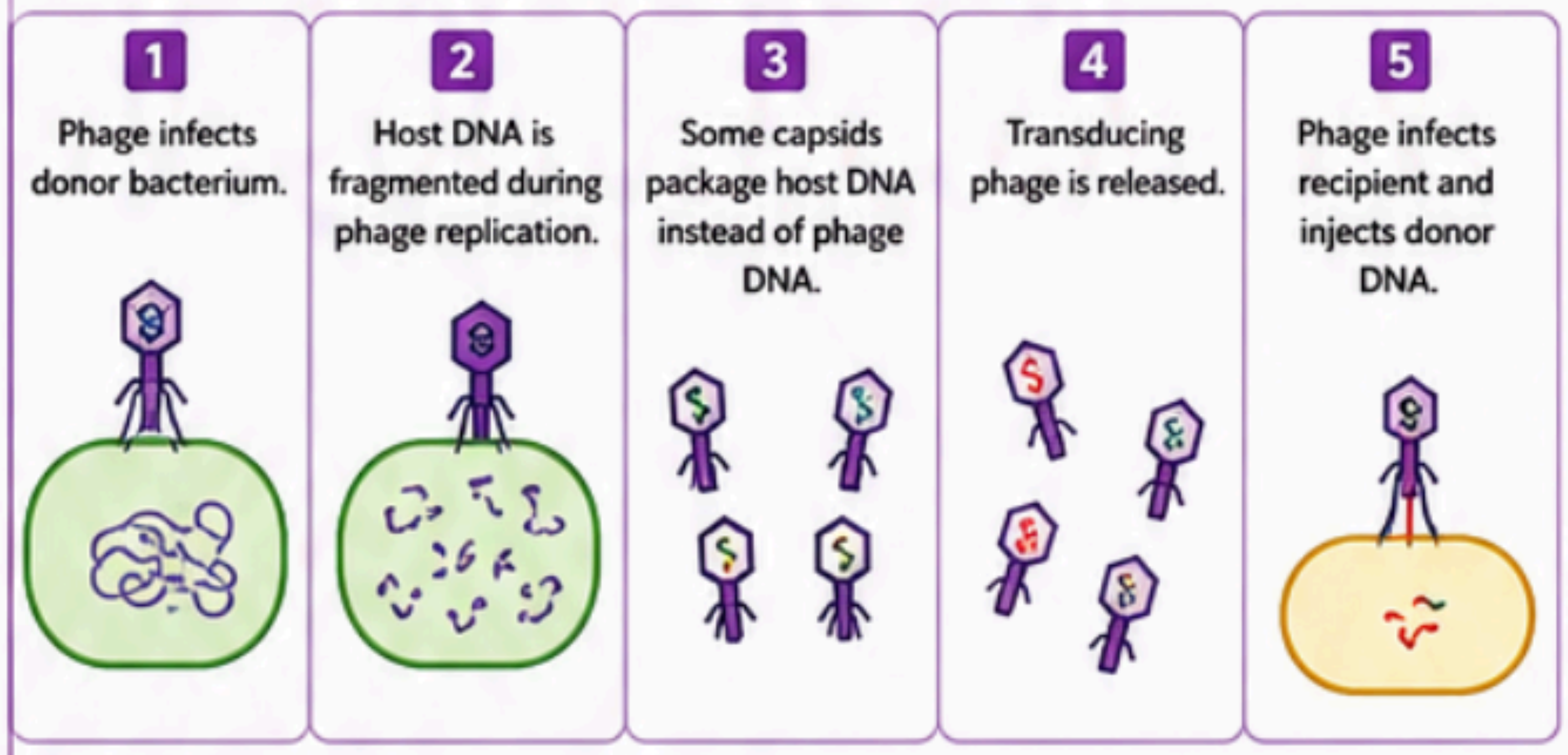
Transduction is the transfer of bacterial DNA from one bacterium to another via bacteriophages (viruses that infect bacteria).

KEY FEATURES

- Mediated by bacteriophages.
- Phage acts as a vector to transfer bacterial genes.
- Two types: Generalized transduction and Specialized transduction.
- Only bacterial DNA is transferred (no plasmid replication cycle).

A. GENERALIZED TRANSDUCTION

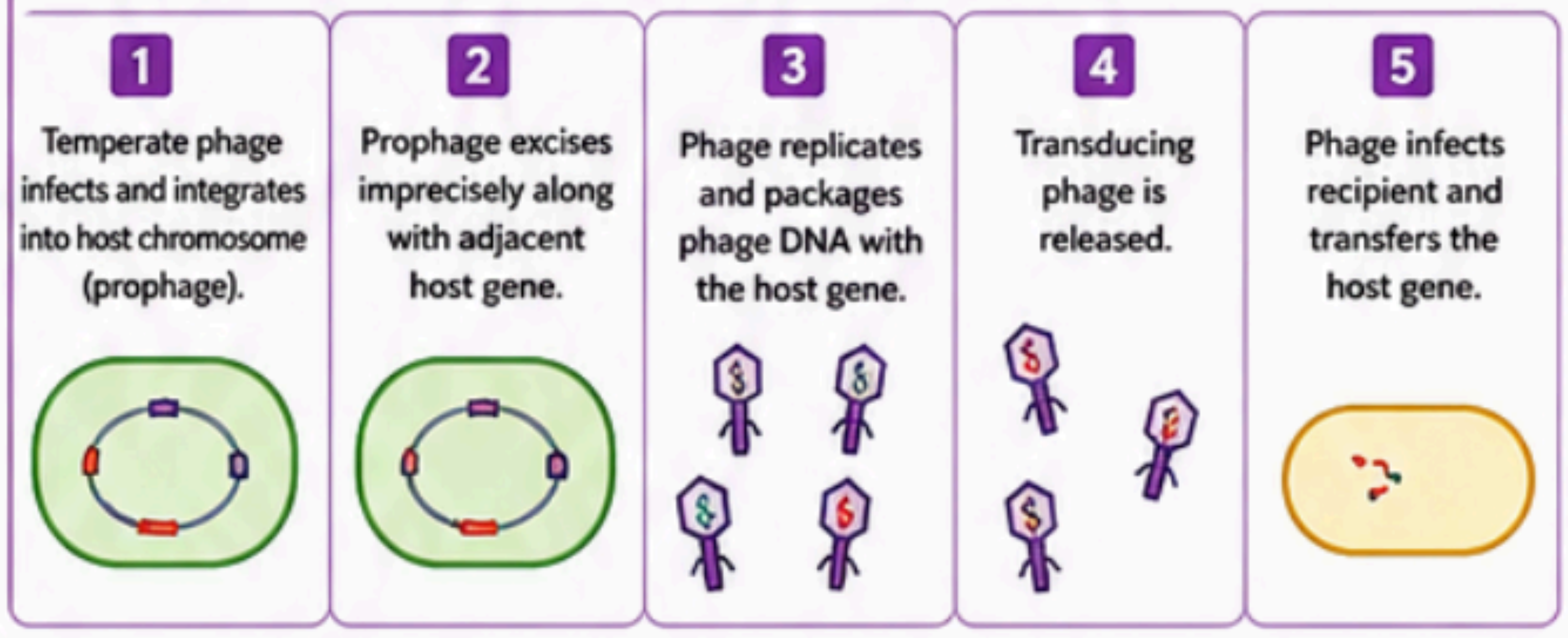
- Any bacterial gene can be transferred.
- Occurs during lytic cycle by packaging of random fragments of host DNA into phage capsid.
- Transducing phage injects donor DNA into recipient.



1. Phage infects donor bacterium.
2. Host DNA is fragmented during phage replication.
3. Some capsids package host DNA instead of phage DNA.
4. Transducing phage is released.
5. Phage infects recipient and injects donor DNA.

B. SPECIALIZED TRANSDUCTION

- Only genes near the prophage integration site are transferred.
- Occurs when temperate phage excises imprecisely from the host chromosome, taking adjacent host genes with it.



1. Temperate phage infects and integrates into host chromosome (prophage).
2. Prophage excises imprecisely along with adjacent host gene.
3. Phage replicates and packages phage DNA with the host gene.
4. Transducing phage is released.
5. Phage infects recipient and transfers the host gene.

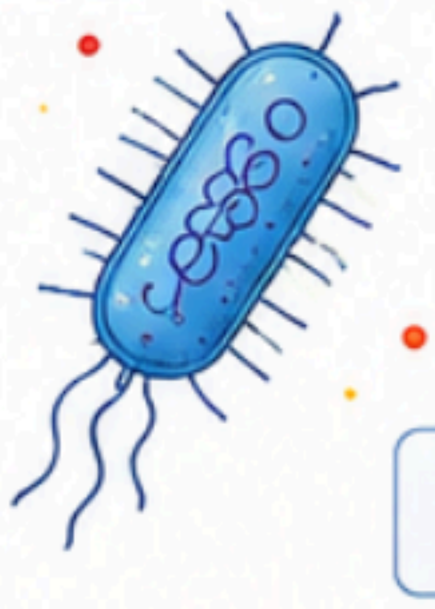
SIGNIFICANCE

- ✓ Major role in bacterial evolution and genetic diversity.
- ✓ Spread of virulence factors, antibiotic resistance, metabolic genes.
- ✓ Used in molecular biology for gene mapping (P1 transduction in *E. coli*).

CONJUGATION vs TRANSDUCTION (At a Glance)

Feature	Conjugation	Transduction
Agent	Conjugative plasmid	Bacteriophage
Requirement	Cell-to-cell contact	Phage infection
DNA transferred	Plasmid & Chromosomal	Only Chromosomal
Transfer mechanism	Pilus-mediated	Phage-mediated
Types	Not applicable	Generalized & Specialized
Example	F plasmid transfer	P1 phage transduction

CONCLUSION: Conjugation and transduction are powerful agents of horizontal gene transfer that promote genetic exchange among bacteria. They enhance adaptability, evolution, and survival in changing environments.



COMPARE THE CELLULAR AND MOLECULAR CHARACTERISTICS OF BACTERIA, ARCHAEA AND EUKARYOTES

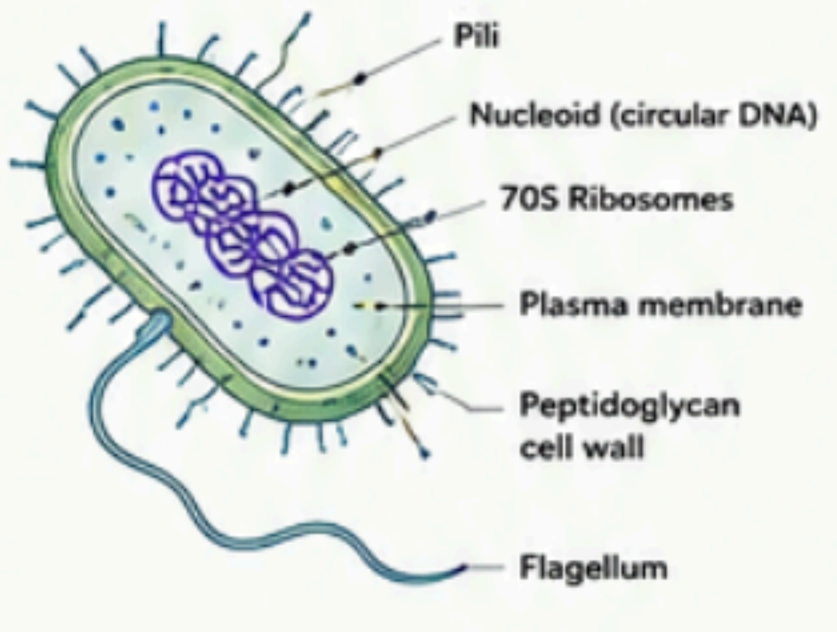
All three domains of life share some fundamental features (DNA as genetic material, ribosomes for protein synthesis, cell membrane, universal genetic code) but differ in many cellular and molecular characteristics.

★ Key: Major differences

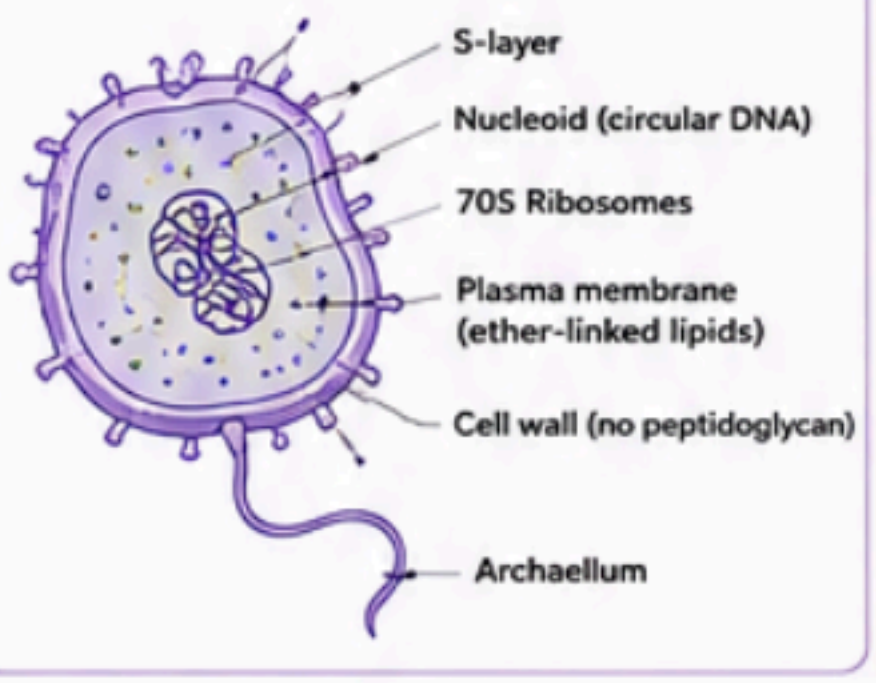
FEATURE	BACTERIA	ARCHAEA	EUKARYOTES
CELLULAR CHARACTERISTICS			
Cell type	★ Prokaryotic (no true nucleus or membrane–bound organelles)	★ Prokaryotic (no true nucleus or membrane–bound organelles)	★ Eukaryotic (true nucleus and membrane–bound organelles)
Cell size	0.5 – 5 μm	0.5 – 5 μm	10 – 100 μm
Cell wall	★ Present in most Peptidoglycan (murein)	★ Present in most No peptidoglycan; pseudopeptidoglycan (S-layers) or other polysaccharides	★ Present in plants (cellulose) and fungi (chitin); absent in animals and protists
Cell membrane lipids	★ Ester-linked fatty acids (phospholipids)	★ Ether-linked isoprenoid chains (often branched) on glycerol-1-phosphate	★ Ester-linked fatty acids (phospholipids) on glycerol-3-phosphate
Membrane sterols	Generally absent (except in some mycoplasmas)	Generally absent (some archaea have unique sterols)	★ Present (e.g., cholesterol in animals, ergosterol in fungi)
Intracellular organization	★ No membrane-bound organelles; 70S ribosomes; may have inclusion bodies	★ No membrane-bound organelles; 70S ribosomes; inclusion bodies (gas vesicles, granules)	★ Membrane-bound organelles (nucleus, mitochondria, ER, Golgi, lysosomes, chloroplasts in plants); 80S ribosomes (cytoplasm)
Cytoskeleton	Simple (e.g., FtsZ)	Simple (e.g., FtsZ homologs)	★ Well-developed (microtubules, microfilaments, intermediate filaments)
Flagella / Motility	★ Simple flagella (flagellin); rotary movement	★ Archaella (not made of flagellin); rotary movement	★ Complex flagella (9+2 microtubule arrangement); whip-like movement
Reproduction	Asexual (binary fission); genetic exchange by HGT	Asexual (binary fission); genetic exchange by HGT	★ Asexual (mitosis) and sexual (meiesis and fertilization)
Examples	*Escherichia coli, Bacillus subtilis, Cyanobacteria*	*Methanobacterium, Halobacterium, Sulfolobus*	Animals, Plants, Fungi, Protists
MOLECULAR CHARACTERISTICS			
Genetic material	Circular dsDNA; usually single chromosome; plasmids common	Circular dsDNA; usually single chromosome; plasmids present	★ Linear dsDNA; multiple chromosomes with histones
Histone proteins	★ Absent	★ Present (histone-like proteins with archaeal features)	★ Present (core histones H2A, H2B, H3, H4; eukaryotic type)
Typical genome size	0.5 – 10 Mbp	0.5 – 6 Mbp	★ 10 – >100,000 Mbp
Introns	Rare	Rare	★ Common
Ribosomes	70S (30S + 50S)	70S (30S + 50S)	★ 80S (40S + 60S) in cytoplasm
Transcription	One RNA polymerase; simple promoters (-10, -35 boxes)	★ Multiple RNA polymerases; promoter elements similar to eukaryotes (TATA box, etc.)	★ Multiple RNA polymerases (I, II, III); complex transcription machinery
mRNA processing	★ Minimal (no capping, splicing, or poly-A tail)	Minimal (rare introns; limited processing)	★ Extensive (5′ capping, splicing, 3′ poly-A tail)
Translation initiation	Shine–Dalgarno sequence for ribosome binding	Shine–Dalgarno-like sequence or leaderless mRNA	★ 5′ cap-dependent scanning (Kozak sequence)
tRNA	Simple structures; limited modifications	Complex; many unique modifications	★ Complex; many modifications
Response to antibiotics	Many are sensitive to common antibiotics	★ Generally resistant to antibiotics that target bacteria	★ Generally not affected by prokaryotic antibiotics
Unique molecular features	Peptidoglycan cell wall; formylated Met in proteins	★ Ether lipids; unique coenzymes (methanogenesis, extremozymes)	★ Complex signaling pathways; protein modifications (phosphorylation, glycosylation)

CELL STRUCTURE AT A GLANCE (Not to Scale)

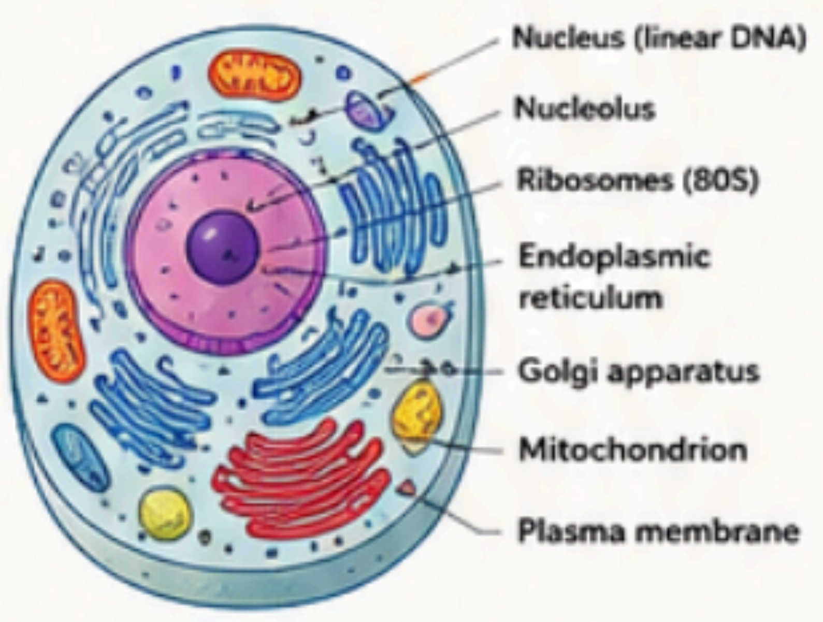
BACTERIA (Prokaryote)



ARCHAEA (Prokaryote)


S-layer
Nucleoid (circular DNA)
70S Ribosomes
Plasma membrane (ether-linked lipids)
Cell wall (no peptidoglycan)
Archaellum

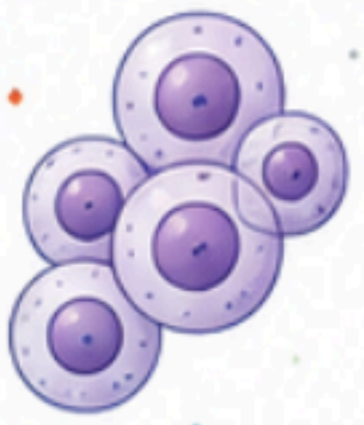
EUKARYOTE



SUMMARY

- Bacteria and Archaea are prokaryotes; Eukaryotes have a true nucleus and organelles.
- Cell wall composition, membrane lipids, and genetic machinery show clear differences.
- Molecular systems of Archaea are more similar to Eukaryotes than to Bacteria in some aspects.
- These differences reflect distinct evolutionary lineages and adaptations.

CONCLUSION: While all life forms share core biological principles, Bacteria, Archaea and Eukaryotes differ significantly in cellular architecture and molecular machinery, underlying their diverse lifestyles and evolutionary histories.



DISCUSS THE ORIGIN OF MULTICELLULARITY AND EVOLUTION OF BILATERAL SYMMETRY IN ANIMALS

Multicellularity: The condition in which many cells work together as a coordinated unit, showing division of labour and intercellular communication.

Bilateral symmetry: Body plan with one plane dividing the body into left and right mirror-image halves.

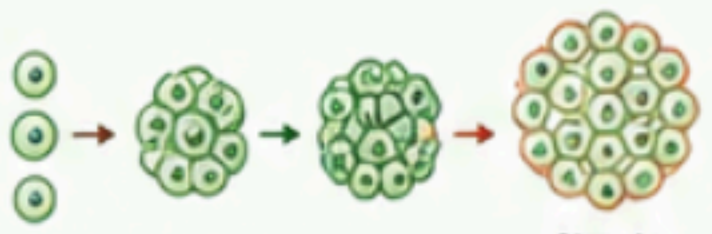
1 ORIGIN OF MULTICELLULARITY IN ANIMALS

Multicellularity evolved independently many times, but in animals it arose once in the common ancestor of **Metazoa ~ 600–800 million years ago (Ediacaran period)**. The transition from unicellular to multicellular life was gradual.

HYPOTHESES FOR THE ORIGIN

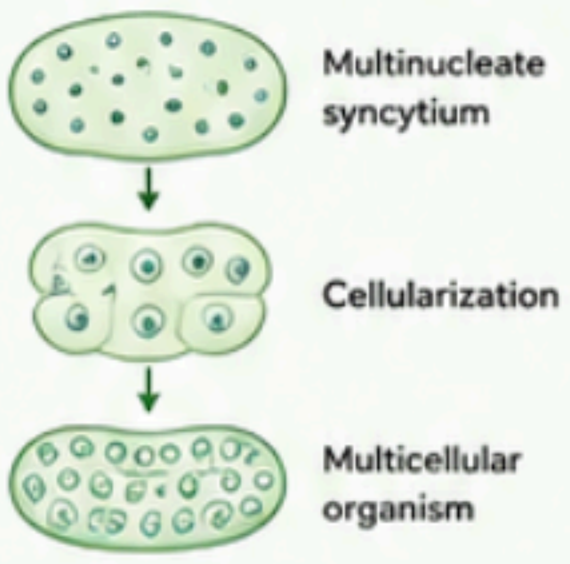
1 Colonial hypothesis (Most widely accepted)

- Cells of a colonial organism became increasingly specialised and integrated.
- Division of labour improved efficiency.
- Incomplete separation of daughter cells after division led to cell adhesion and communication.



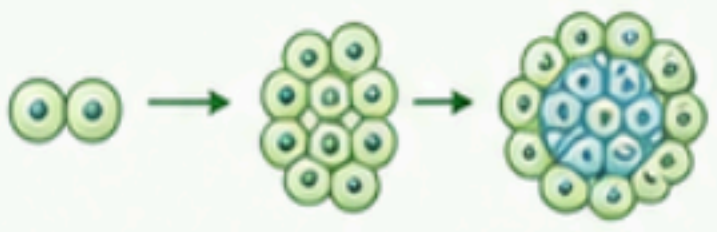
2 Syncytial hypothesis

- A large multinucleate syncytium arose due to repeated nuclear divisions without cell division.
- Cell membranes later formed around nuclei leading to cellularization.



3 Symplasmic (Clonal) hypothesis

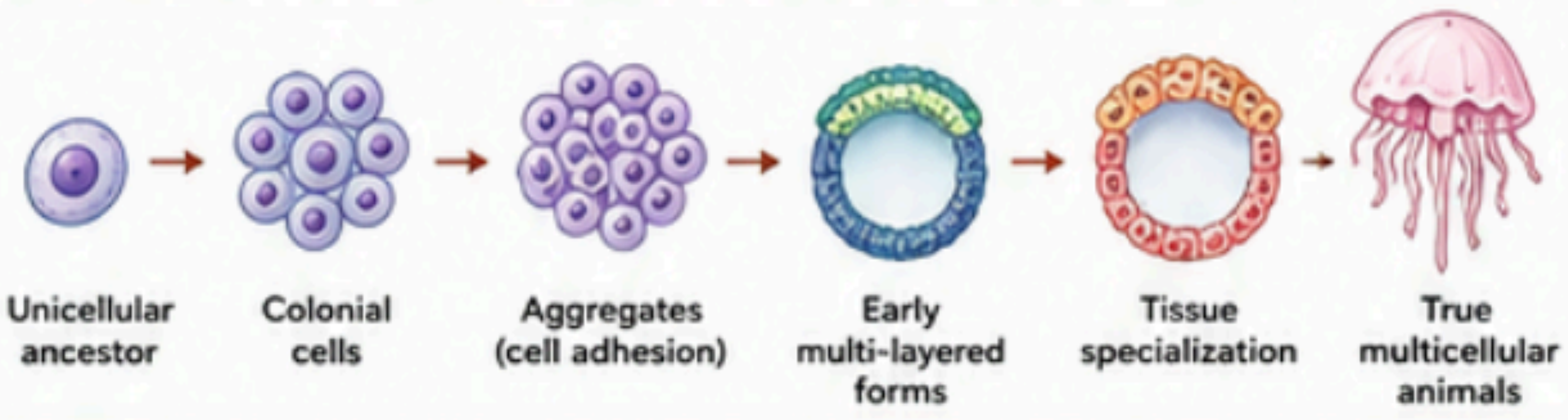
- Repeated mitotic divisions in a common extracellular matrix produced a clonal aggregate of cells.
- Gradual change from independent to interdependent cells.



KEY DRIVERS / ADVANTAGES

- ✓ Increased cell number and size → better resource acquisition and defense.
- ✓ Specialization of cells → division of labour (digestive, protective, reproductive).
- ✓ Cellular communication and adhesion → coordination.
- ✓ Evolution of extracellular matrix and cell–cell junctions.
- ✓ Development of genomes and regulatory genes (e.g., Hox genes, cadherins, signaling pathways) controlling differentiation.

STAGES IN THE EVOLUTION OF MULTICELLULAR ANIMALS


Unicellular ancestor
Colonial cells
Aggregates (cell adhesion)
Early multi-layered forms
Tissue specialization
True multicellular animals

EVIDENCE

- Fossil record: Ediacaran biota (e.g., *Dickinsonia, Rangea*) shows simple multicellular organisms.
- Comparative studies of sponges (Porifera) – simplest animals with cellular level organization.
- Molecular evidence: Conservation of developmental genes (Hox, Pax, Wnt, Notch) in metazoans.

2 EVOLUTION OF BILATERAL SYMMETRY IN ANIMALS

Bilateral symmetry is a hallmark of most animals (except some sponges, cnidarians and adult echinoderms). It evolved early in animal history and provided a major advantage for active life.

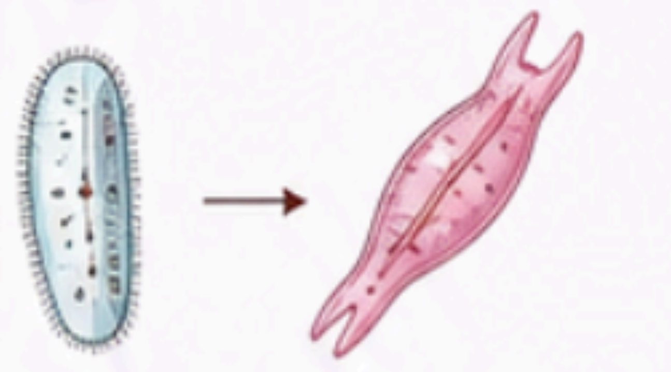
ORIGIN AND EVOLUTION

1. Ancestral condition: Early animals were mostly asymmetrical (sponges) or radially symmetrical (cnidarians, ctenophores).
2. Bilateral symmetry likely evolved in small, actively moving, bottom-dwelling animals during the Ediacaran–Cambrian transition (~600 Ma).
3. Provides **cephalization** (concentration of sense organs and nervous tissue **at anterior end**) and **directional movement.**
4. Associated with the evolution of a centralized nervous system and complex organs.

HYPOTHESES FOR THE ORIGIN

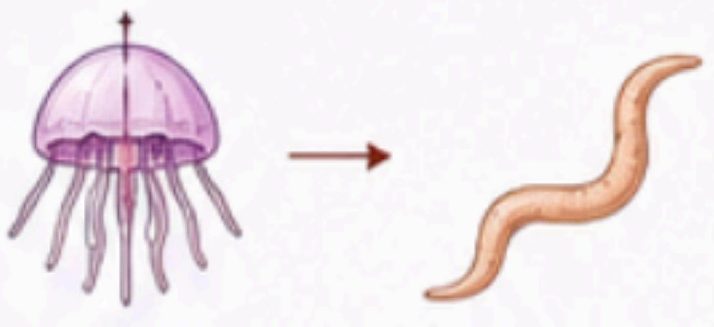
1 Planuloid hypothesis

Larval forms of cnidarians (planula) are bilaterally symmetrical. Adult forms evolved from planula-like ancestors.



2 Convergence hypothesis

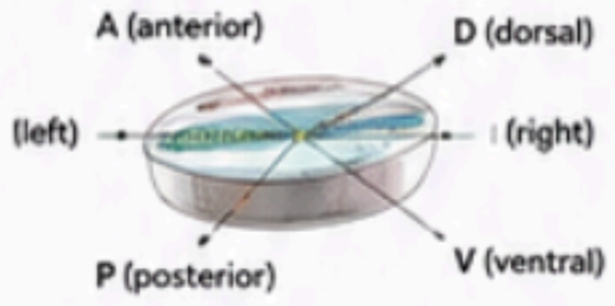
Bilateral symmetry evolved independently in bilaterians due to similar selective pressures for active life.



HOW BILATERAL SYMMETRY EVOLVED: KEY STEPS

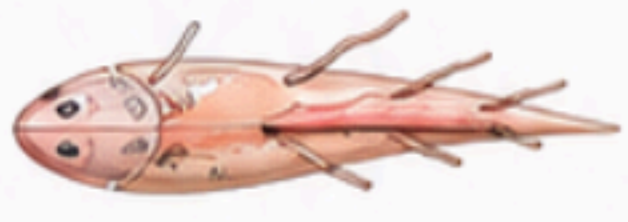
1 Establishment of body axes

Molecular cues (e.g., Wnt, Nodal, BMP) set up antero-posterior (A–P), dorsal–ventral (D–V) and left–right (L–R) axes.



2 Cephalization

Concentration of sensory cells and nervous tissue at anterior end (forms a 'head').

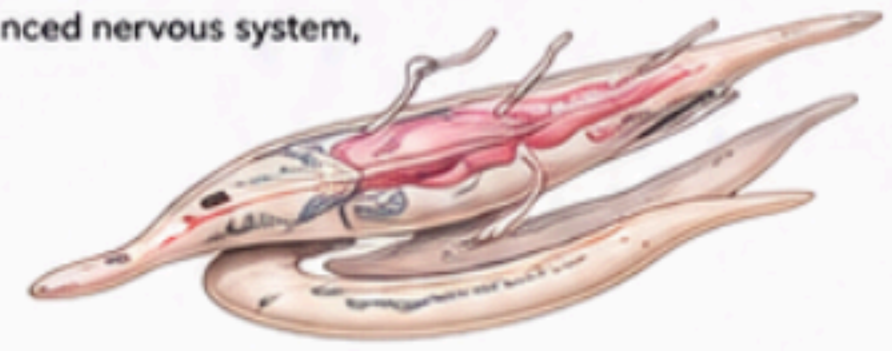


3 Evolution of locomotion

Musculature and coordinated movement developed; bilaterally symmetric body allows efficient directional locomotion.

4 Organ system complexity

Development of a through gut, advanced nervous system, excretory and circulatory systems.



COMPARISON AT A GLANCE

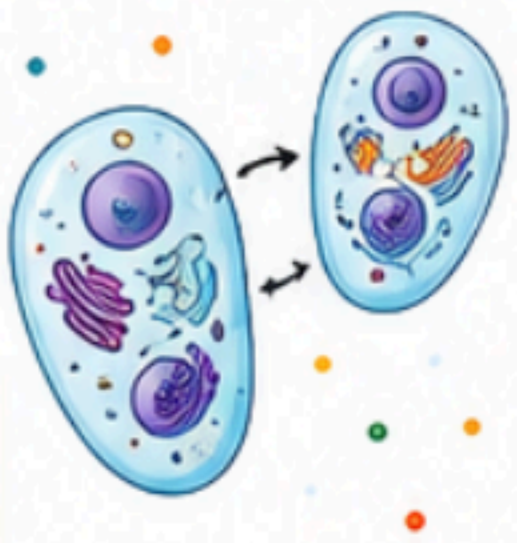
Feature	Asymmetrical / Unicellular	Radial Symmetry (Cnidarians)	Bilateral Symmetry (Bilaterians)
Body plan	No definite shape	Body parts arranged around central axis	One plane divides left and right halves
Movement	Mostly passive	Limited direction	Active, directional
Nervous system	Diffuse or absent	Nerve net	Centralized (brain, nerve cords)
Cephalization	Absent	Absent	Present (head region)
Digestion	Intracellular / simple	Gastrovascular cavity (one opening)	Complete digestive tract (mouth and anus)
Examples	Protists	Hydra, Jellyfish, Sea anemone	Flatworms, Annelids, Arthropods, Vertebrates

SIGNIFICANCE

- ✓ Multicellularity allowed larger size, specialization, and complex behaviours.
- ✓ Bilateral symmetry increased efficiency in movement, feeding, sensory perception and survival.
- ✓ Led to the radiation of diverse animal phyla in the Cambrian explosion.

CONCLUSION: Multicellularity in animals arose from simple ancestors through increased cell cooperation, division of labour and genetic control of development. Bilateral symmetry evolved from earlier body plans, enabling cephalization and active life, which together paved the way for the great diversity of animals today.

DESCRIBE THE CONSEQUENCES OF GENOME AND GENE DUPLICATIONS

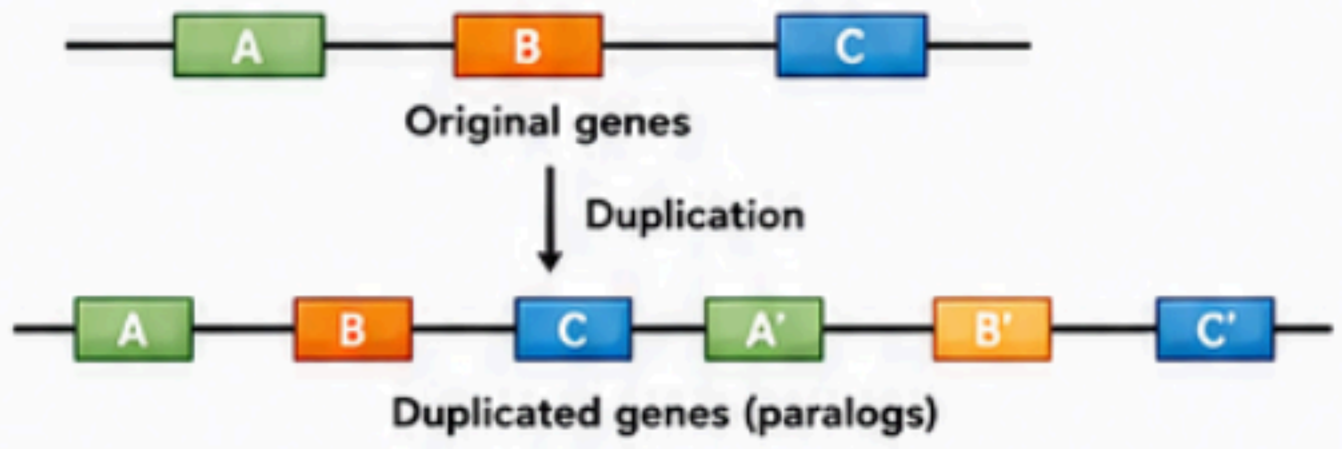


Duplication is the process by which DNA segments (genes or whole genomes) are copied, producing additional genetic material. The extra copies provide raw material for evolution and have far-reaching consequences at **molecular, cellular, organismal and evolutionary levels.**

1 WHAT ARE GENOME AND GENE DUPLICATIONS?

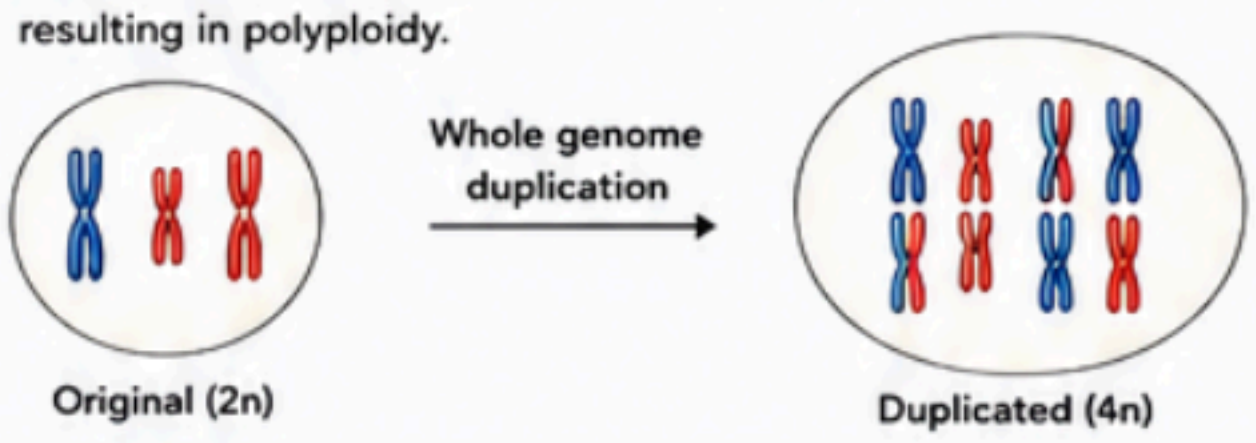
A. GENE DUPLICATION

- A segment of DNA containing one or more genes is copied. Duplicates may lie next to the original (tandem) or at different locations in the genome.



B. GENOME DUPLICATION

- The entire set of chromosomes is duplicated, resulting in polyploidy.



TYPES OF GENOME DUPLICATION

- **Autopolyploidy** – duplication within the same species.
- **Allopolyploidy** – duplication after hybridization between different species.
- **Segmental/partial duplication** – duplication of large chromosomal segments.

MECHANISMS CAUSING DUPLICATIONS

- Unequal crossing over during meiosis
- Replication slippage
- Transposon-mediated duplication
- Retrotransposition (gene copy via RNA intermediate)
- Whole genome duplication (errors in cell cycle)

FATES OF DUPLICATED GENES (AFTER DUPLICATION)

Nonfunctionalization (pseudogenization)	One copy accumulates deleterious mutations and becomes a pseudogene.
Neofunctionalization	One copy acquires a new beneficial function.
Subfunctionalization	Both copies divide the original function (partitioning).
Dosage balance	Both copies maintain the same function to retain proper gene dosage.
Loss	Duplicate is deleted from the genome over time.

2 MAJOR CONSEQUENCES OF GENOME AND GENE DUPLICATIONS

1 Increased genetic material and redundancy

- Extra copies increase DNA content of genomes.
- Provide backup copies, so loss-of-function mutations in one copy may not be lethal.

Example

Humans have ~2× more DNA than strictly needed for basic gene functions.

2 Functional innovation (neofunctionalization)

- Duplicated genes are free from strong purifying selection.
- One copy acquires beneficial mutations that lead to new functions.

Example

Vertebrate vision genes (opsins) duplicated and evolved to detect different wavelengths of light.

3 Subfunctionalization (division of labour)

- Both copies retain parts of the original function.
- Each copy specializes in a subset of the ancestral role.

Example

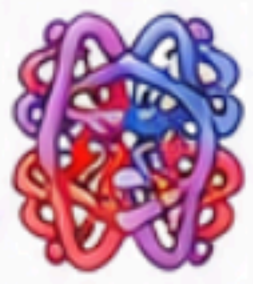
Duplicated genes for digestive enzymes in mammals show tissue-specific expression (pancreas vs. intestine).

4 Gene family expansion

- Repeated duplications build large gene families.
- Leads to greater complexity and adaptability.

Example

Globin gene family (α, β, γ, δ, ε) arose from duplication events.



5 Evolution of novel pathways and networks

- Duplicated genes can combine or interact in new ways.
- Contributes to the evolution of new metabolic or regulatory pathways.

Example

Duplication of genes in the phenylpropanoid pathway led to diverse plant secondary metabolites.

6 Increased organismal complexity

- More genes and regulatory elements enable development of complex structures and body plans.
- Often seen after whole genome duplications.

Example

Many rounds of whole genome duplication in early vertebrates contributed to complexity of organs and systems.

7 Polyploidy-related consequences (genome duplication)

- May cause increased cell size (gigas effect).
- Heterosis (hybrid vigor) in plants.
- Can lead to reproductive isolation and speciation.
- In plants, results in greater size, stress tolerance, and novel traits.

Example

Wheat (*Triticum aestivum*) is an allohexaploid ($6n = 42$) and more productive than its diploid ancestors.

8 Potential deleterious effects

- Increased DNA to replicate and maintain (metabolic cost).
- Gene dosage imbalance may disrupt cellular networks.
- Some duplicates become nonfunctional.

Example

Not all duplicates are useful; many become pseudogenes or are lost.

3 EVIDENCE FOR DUPLICATION AND ITS CONSEQUENCES

Comparative genomics

Many paralogous genes present in clusters or blocks across species.

Fossil record

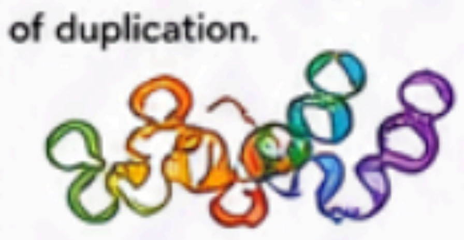
Radiations of organism groups often follow periods of genome duplication.

Cytogenetics

Polyploidy observed in many plants and some animals.

Molecular examples

Gene families (e.g., MHC, HOX, globin, olfactory receptors) show signatures of duplication.



4 IMPORTANCE OF DUPLICATIONS IN EVOLUTION

- Provide raw material for evolutionary innovation.
- Enable adaptation to new environments and niches.
- Drive biodiversity and complexity of life.
- Central to major evolutionary transitions.

SUMMARY

Genome and gene duplications increase genetic content and create extra copies of genes. These duplicates may be preserved, partitioned, modified or lost, leading to new functions, complex traits, polyploidy, and increased biodiversity. Although sometimes deleterious, duplication is a powerful engine of evolution.

DEFINE THE FOLLOWING

(a) Pseudogene (b) Genetic drift (c) Cladogenesis (d) Biosystematics

(a) PSEUDOGENE

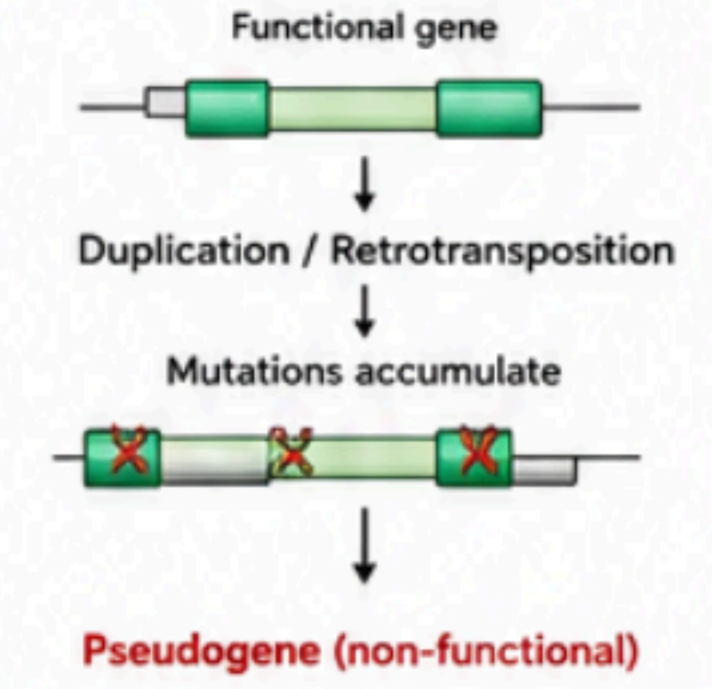
DEFINITION:

A pseudogene is a DNA sequence that closely resembles a functional gene but has lost its ability to produce a functional protein due to mutations such as insertions, deletions or premature stop codons.

CHARACTERISTICS

- ✓ Non-functional copy of a gene.
- ✓ Does not produce active proteins.
- ✓ Show high sequence similarity to functional genes.
- ✓ Often transcribed but not translated to functional proteins.

HOW PSEUDOGENES ARISE



Functional gene

↓

Duplication / Retrotransposition

↓

Mutations accumulate

↓

Pseudogene (non-functional)

TYPES

1. **Processed pseudogenes**
   – Formed from reverse-transcribed mRNA; lack introns.
2. **Unprocessed pseudogenes**
   – Arise by duplication of a gene followed by mutations; retain introns.
3. **Unitary pseudogenes**
   – Formed when a single-copy gene becomes non-functional without duplication.

SIGNIFICANCE

- Provide evidence for evolution and common ancestry.
- Help in understanding the evolution of gene families.
- May regulate expression of functional genes (e.g., act as miRNA sponges, regulatory RNAs).
- Useful in identifying genes and studying genome organization.

EXAMPLE Human GULO pseudogene (L-gulonolactone oxidase gene): mutants in this pseudogene explain why humans cannot synthesize vitamin C, unlike most other mammals.

(b) GENETIC DRIFT

DEFINITION:

Genetic drift is the random change in allele frequencies in a population from one generation to the next due to chance events rather than natural selection.

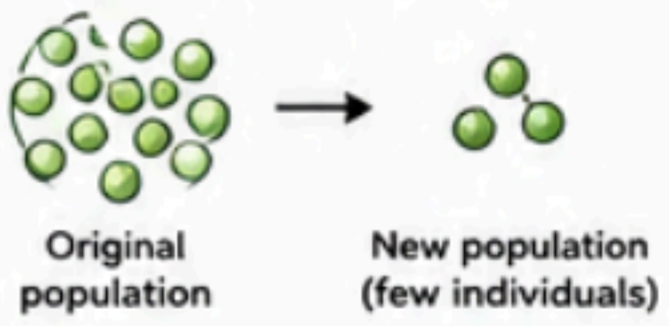
CHARACTERISTICS

- ✓ More pronounced in small populations.
- ✓ Can cause loss or fixation of alleles.
- ✓ Reduces genetic variation over time.
- ✓ Non-adaptive; acts by chance.

TYPES

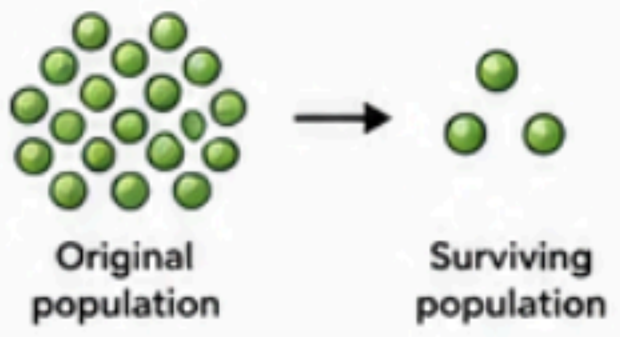
1. Founder effect

A new population is established by a few individuals carrying only a small part of the genetic variation of the original population.



2. Bottleneck effect

A large population is drastically reduced in size by a disaster, disease, or other event.



CONSEQUENCES

- Decrease in genetic diversity.
- Increased inbreeding and homozygosity.
- Loss of rare alleles; fixation of some alleles.
- May lead to differentiation among populations.
- Can influence evolution by random processes.

EXAMPLE High frequency of genetic disorders such as Tay–Sachs disease in isolated populations (Ashkenazi Jews); variation in beak size in small bird populations.

(c) CLADOGENESIS

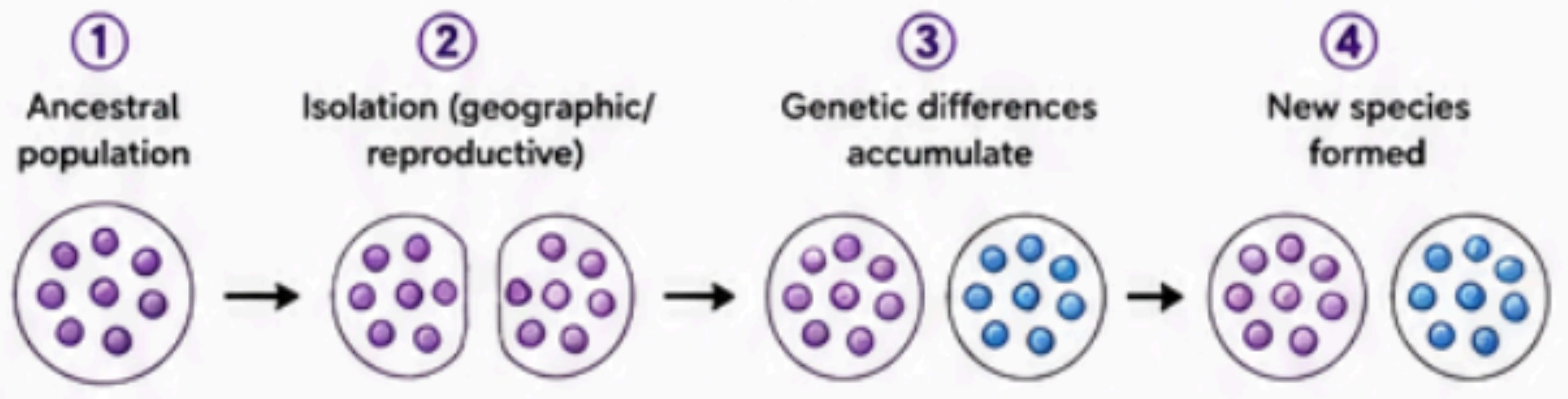
DEFINITION:

Cladogenesis is the evolutionary process by which one ancestral species splits into two or more descendant species, leading to the formation of new evolutionary lineages.

CHARACTERISTICS

- ✓ Results in increasing biodiversity.
- ✓ Occurs due to reproductive or geographic isolation.
- ✓ Leads to divergent evolution.
- ✓ Produces branching patterns in phylogenetic trees.

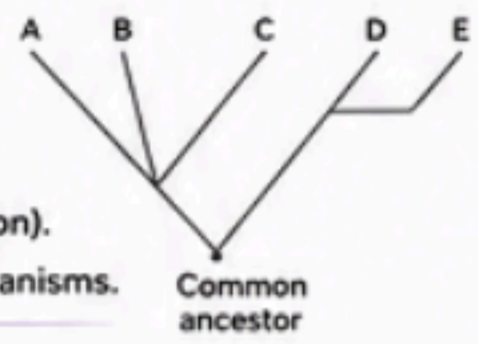
PROCESS



① Ancestral population → ② Isolation (geographic/ reproductive) → ③ Genetic differences accumulate → ④ New species formed

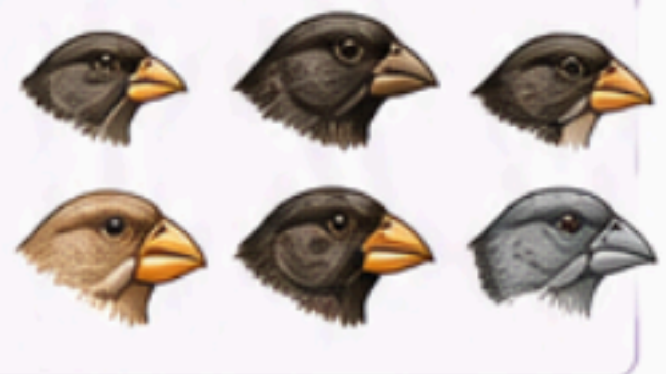
IMPORTANCE

- Major mechanism of speciation.
- Explains adaptive radiation and the origin of many groups.
- Phylogenetic trees are based on cladogenesis (branching evolution).
- Helps in understanding the evolutionary relationships among organisms.



EXAMPLE

Darwin's finches on the Galápagos Islands evolved from a common ancestor into multiple species with different beak shapes, diets and habitats.

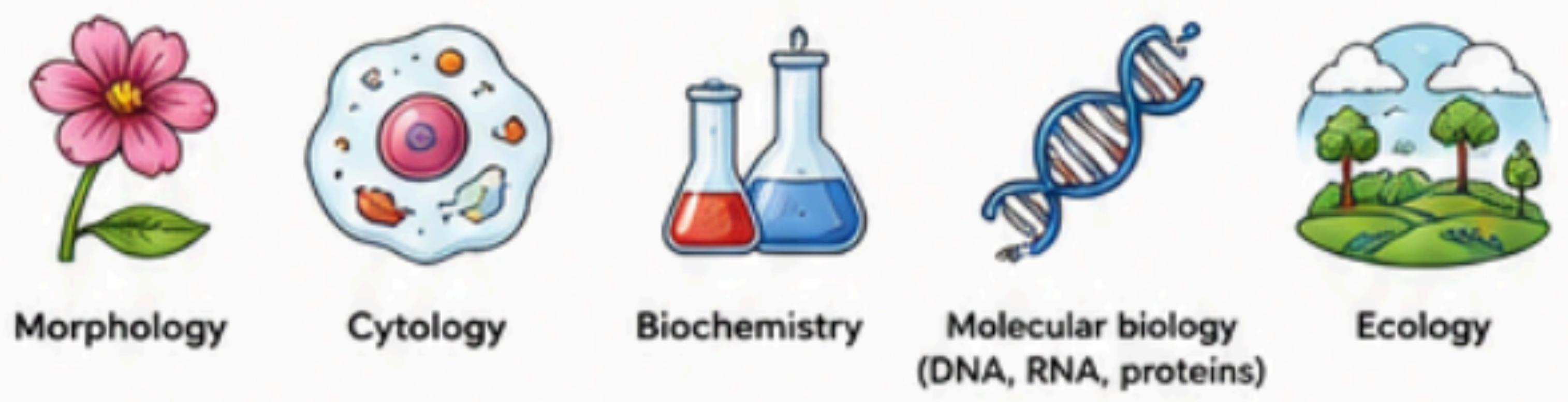


(d) BIOSYSTEMATICS

DEFINITION:

Biosystematics is the branch of biology that deals with the classification and identification of organisms based on the study of their evolutionary relationships using all available evidence (morphological, cytological, biochemical, molecular, ecological, etc.).

APPROACH / TOOLS USED



IMPORTANCE

- Provides a natural classification reflecting evolutionary relationships.
- Helps in accurate identification of species, including cryptic (morphologically similar) species.
- Essential for biodiversity conservation.
- Useful in agriculture, medicine, forensics, and biotechnology.

KEY FEATURES

- ✓ Integrates data from multiple disciplines.
- ✓ Uses modern techniques (e.g., DNA sequencing, phylogenetics, cladistics).
- ✓ Continuously updated with new information.

EXAMPLE

DNA barcoding uses a standard region of DNA (e.g., rbcL in plants, COI in animals) to identify species and resolve taxonomic relationships.

COI-5P658

OUTCOMES

- Construction of phylogenetic trees.
- Understanding of evolutionary pathways.
- Reclassification when new evidence is obtained.

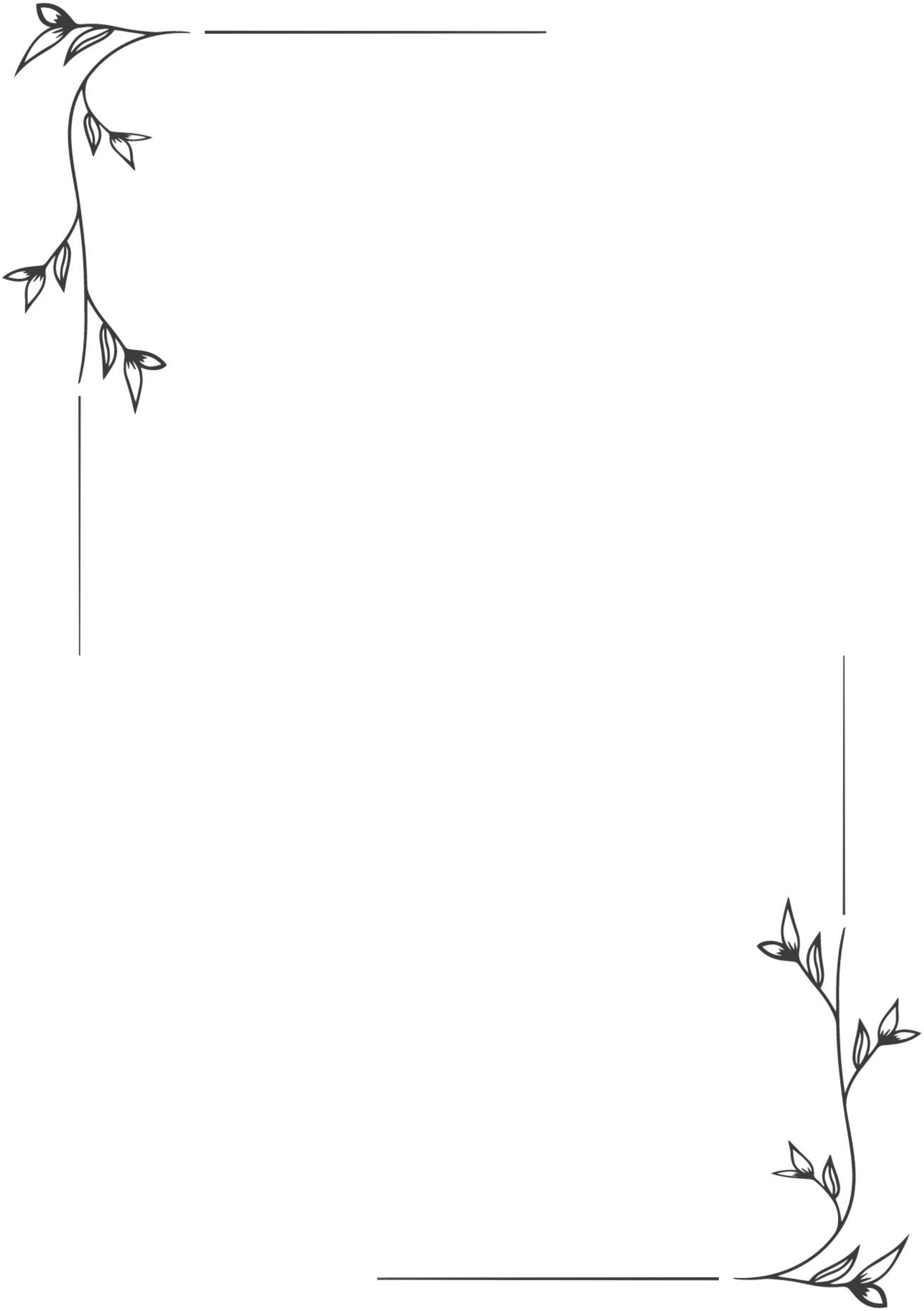
SUMMARY

Pseudogene: A non-functional gene-like sequence formed by mutations; provides clues to evolution.

Genetic drift: Random change in allele frequencies causing variation loss or fixation.

Cladogenesis: Branching evolution where one species splits into two or more new species.

Biosystematics: Scientific classification of organisms using all evidence to understand evolutionary relationships.



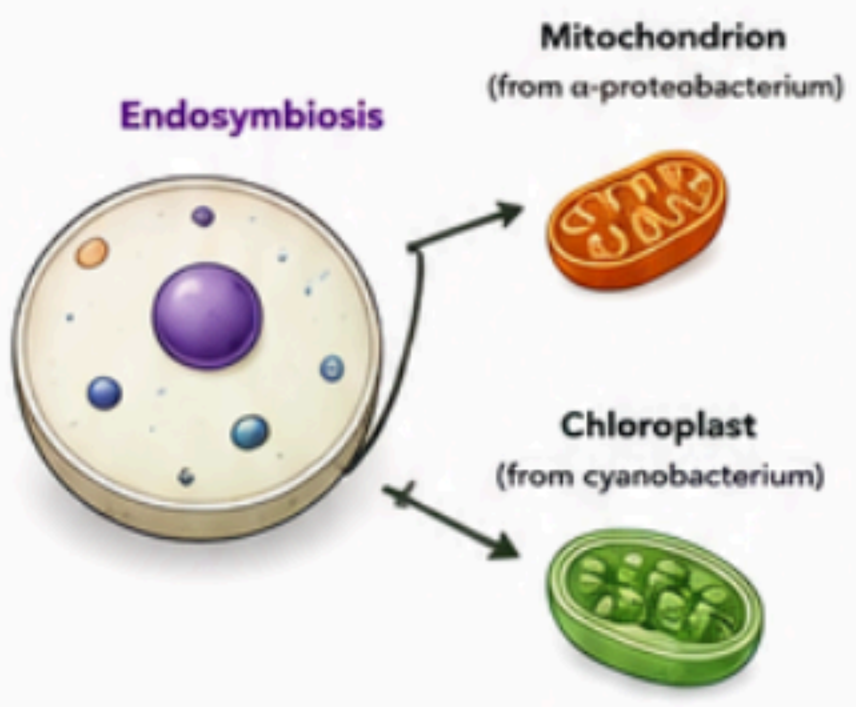
6. THE THEORY OF ENDOSYMBIOSIS

How Mitochondria and Chloroplasts Arose in Eukaryotes

The endosymbiotic theory proposes that certain organelles in eukaryotic cells—mitochondria and chloroplasts—originated as free-living prokaryotes that were engulfed by an ancestral host cell and evolved a mutualistic (symbiotic) relationship.

1. THE ENDOSYMBIOTIC THEORY: OVERVIEW

- ☑ Proposed independently by Lynn Margulis (1967) based on earlier ideas by K. S. Mereschkowski (1905).
- ☑ Explains the origin of mitochondria and chloroplasts as ancient bacteria that took up residence inside a host cell.
- ☑ The relationship evolved from parasitism to mutualism, beneficial for both partner and host.
- ☑ Results in complex eukaryotic cells with new capabilities (aerobic respiration, photosynthesis).



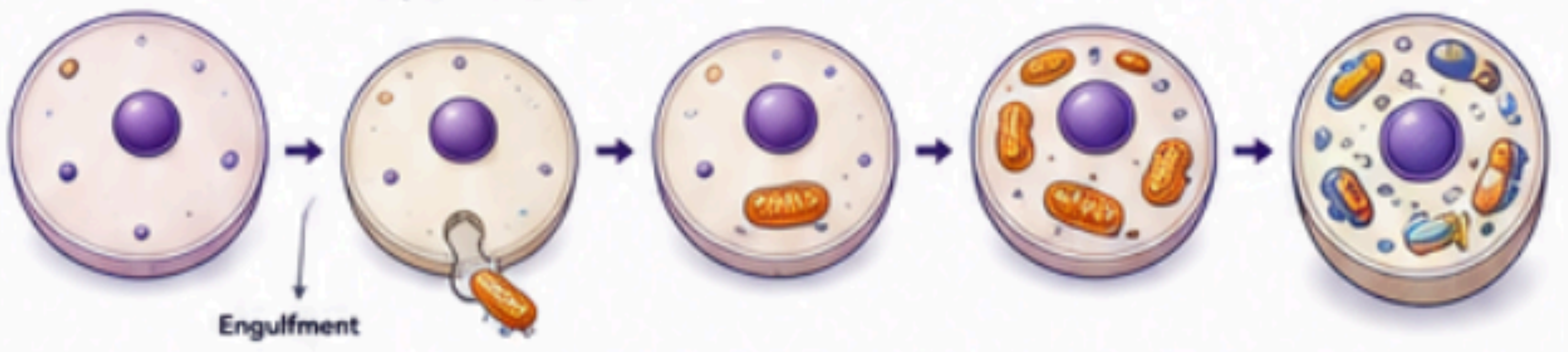
The host cell gained energy efficiency and new metabolic capabilities.

2. EVIDENCE SUPPORTING ENDOSYMBIOSIS

Double Membrane		Both mitochondria and chloroplasts are enclosed by a double membrane, similar to bacteria.
Own Circular DNA		They contain their own circular DNA, like prokaryotes.
70S Ribosomes		Organelles have 70S ribosomes, same as bacteria (cytoplasm has 80S).
Binary Fission		They reproduce by binary fission, independently of the host cell cycle.
Size & Structure		Similar in size to bacteria (1–10 μm) and have prokaryote-like features.
Antibiotic Sensitivity		Sensitive to antibiotics that inhibit bacterial (rather than eukaryotic) processes.
Phylogenetic Evidence		Mitochondria are closely related to α-proteobacteria; chloroplasts to cyanobacteria.

3. PRIMARY ENDOSYMBIOSIS: ORIGIN OF MITOCHONDRIA AND CHLOROPLASTS

3A. ORIGIN OF MITOCHONDRIA (FROM α-PROTEOBACTERIUM)

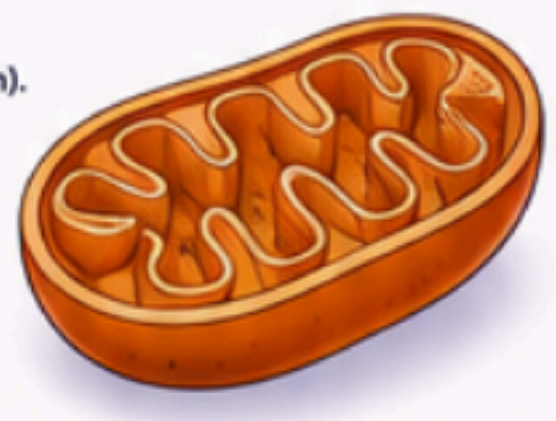


① Ancestral host cell (Domain Eukarya)
② Engulfment of an aerobic bacterium (α-proteobacterium)
③ Establishment of endosymbiosis
④ Integration and co-evolution
⑤ Modern eukaryotic cell with mitochondria

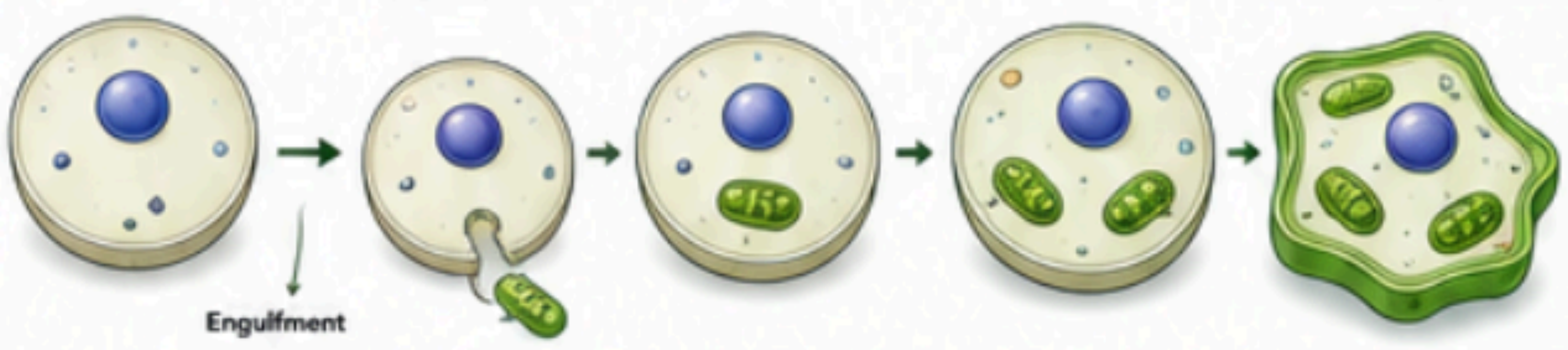
Benefit: Bacterium provided efficient ATP production via aerobic respiration. Host provided protection and nutrients.

Key features of mitochondria today:

- Double membrane (outer from host, inner from bacterium).
- Circular DNA (~16.5 kb in humans).
- 70S ribosomes.
- Reproduce by binary fission.
- Site: matrix.
- Function: ATP production (oxidative phosphorylation).



3B. ORIGIN OF CHLOROPLASTS (FROM CYANOBACTERIUM)

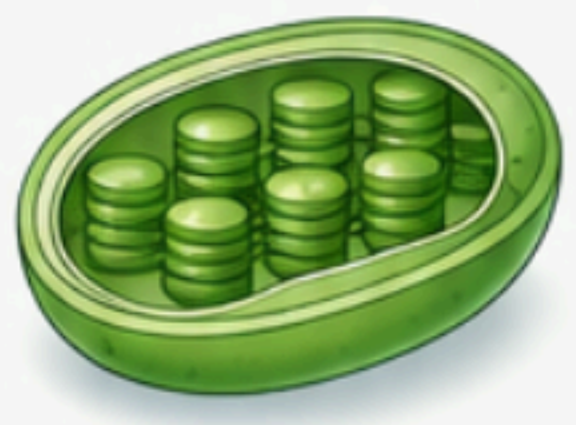


① Eukaryotic host cell (heterotrophic)
② Engulfment of a photosynthetic cyanobacterium
③ Establishment of endosymbiosis
④ Integration and co-evolution
⑤ Modern plant (eukaryotic) cell with chloroplasts

Benefit: Cyanobacterium provided photosynthesis; host provided stability and resources.

Key features of chloroplasts today:

- Double membrane.
- Circular DNA (~120–200 kb in plants).
- 70S ribosomes.
- Reproduce by binary fission.
- Site: stroma.
- Function: Photosynthesis (light reactions in thylakoids, CO_2 fixation in stroma).

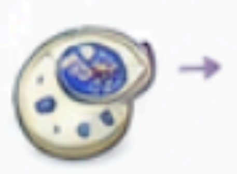


4. GENE TRANSFER TO THE HOST NUCLEUS AND LOSS OF INDEPENDENCE

Gene Transfer (Endosymbiotic Gene Transfer)

① Initially, endosymbiont had its own genome.

② Over evolutionary time, many genes were transferred from the organelle DNA to the host cell nucleus.


③ These genes now encode proteins required for organelle function.

④ The proteins are synthesized in the cytoplasm and imported back into the organelles.

Consequences: Loss of Independence

- Most original genes lost from organelle genomes.
- Organelles cannot survive outside the host cell.
- Depend on nuclear genes for replication, transcription, translation and maintenance.
- Division of organelles synchronized with the host cell cycle.
- Permanent intracellular residency (obligate endosymbionts).

Extent of Gene Transfer

Organelle	Original Genes (Predicted)	Genes Retained Today	% Genes Transferred
Mitochondria	~1000–1500	~37 (humans)	>95%
Chloroplasts	~3000	~80–120 (land plants)	>96%

Example of Gene Functions Now Nuclear-Coded (but act in organelles):

- Enzymes for DNA replication, transcription, and repair
- Proteins of electron transport chain (mitochondria)
- Proteins of photosystems, ATP synthase (chloroplasts)
- Ribosomal proteins and tRNA synthetases

5. EVOLUTIONARY OUTCOMES

- ☑ Greatly increased energy production → allowed evolution of larger, more complex cells.
- ☑ Photosynthesis enabled colonization of light-rich environments and rise of plants and algae.
- ☑ Endosymbiosis is an example of major evolutionary innovation through cooperation.
- ☑ Occurred only once for each organelle (primary endosymbiosis).

One-time events that shaped all eukaryotic life.

6. SUMMARY FLOW

Free-living bacterium (α-proteobacterium or cyanobacterium)
↓
Engulfed by ancestral eukaryote
↓
Survived digestion → endosymbiosis established
↓
Gene transfer to host nucleus
↓
Loss of independence; organelle integration
↓
Modern mitochondria / chloroplasts

7. KEY TAKE-HOME MESSAGES

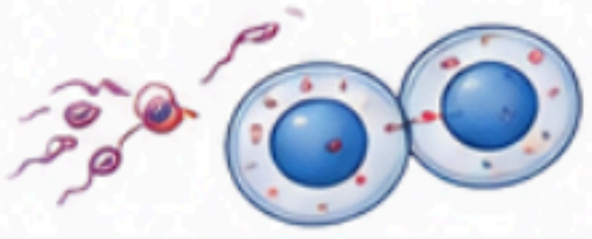
- ☑ Mitochondria originated from α-proteobacteria; chloroplasts from cyanobacteria.
- ☑ Endosymbiosis provided major metabolic advantages for both partners.
- ☑ Most genes transferred to the host nucleus; organelles lost independence.
- ☑ Organelles are now essential, non-autonomous parts of eukaryotic cells.
- ☑ Endosymbiosis is a cornerstone event in the evolution of eukaryotic life.

IN A NUTSHELL

Endosymbiosis turned bacteria into organelles and simple cells into complex life. A story of cooperation that powers every eukaryotic cell.

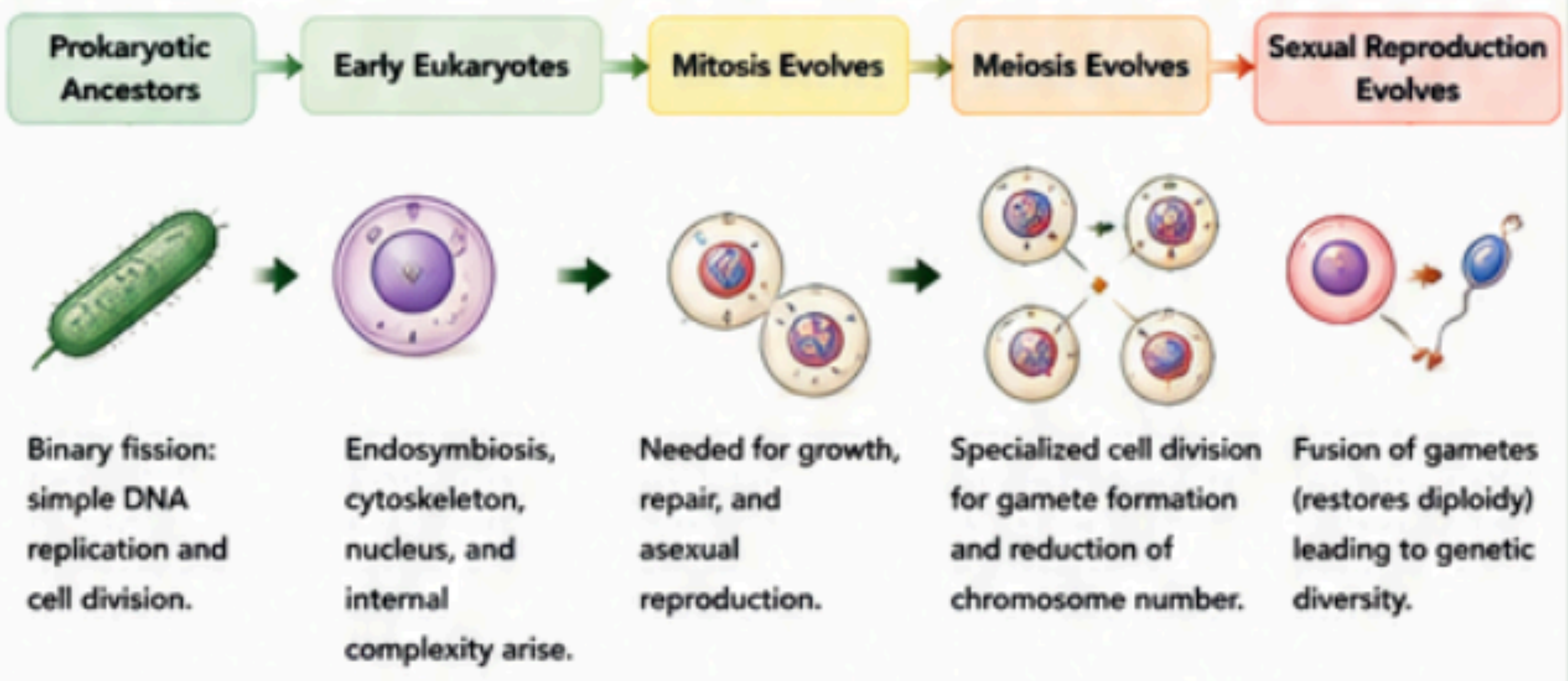
5.(b)

EVOLUTION OF MITOSIS, MEIOSIS AND SEXUAL REPRODUCTION IN EARLY EUKARYOTES



From simple cell division to genetic diversity and survival advantage

1. THE EVOLUTIONARY SEQUENCE: AN OVERVIEW



Prokaryotic Ancestors → Early Eukaryotes → Mitosis Evolves → Meiosis Evolves → Sexual Reproduction Evolves

Prokaryotic Ancestors	Early Eukaryotes	Mitosis Evolves	Meiosis Evolves	Sexual Reproduction Evolves
Binary fission: simple DNA replication and cell division.	Endosymbiosis, cytoskeleton, nucleus, and internal complexity arise.	Needed for growth, repair, and asexual reproduction.	Specialized cell division for gamete formation and reduction of chromosome number.	Fusion of gametes (restores diploidy) leading to genetic diversity.

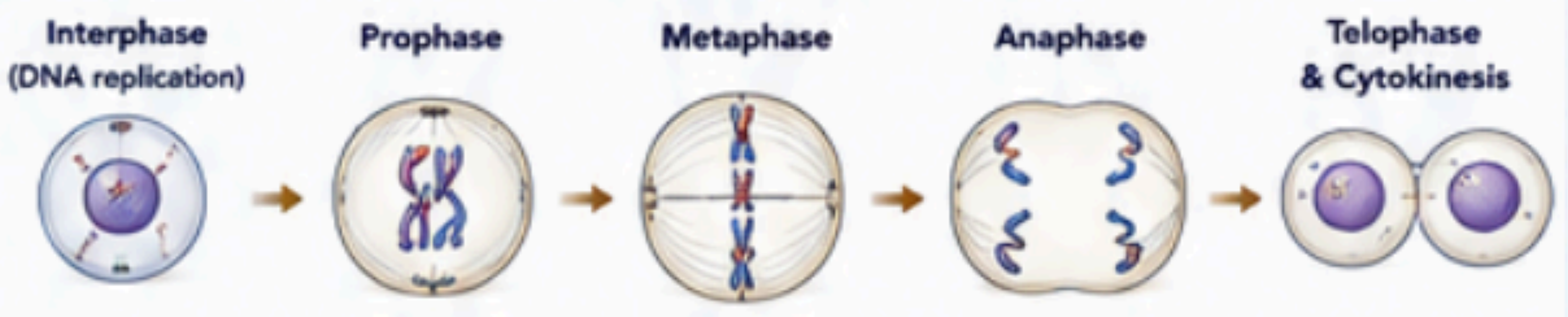
Increasing complexity → genome protection → genetic variation → evolutionary success

2. HOW MITOSIS EVOLVED

Mitosis likely evolved in early eukaryotes to manage larger genomes and complex cell structures.

- From prokaryotic-like DNA replication and septation to orchestrated stages of mitosis.
- Development of cytoskeleton (microtubules, actin) enabled chromosome segregation.
- Mitosis allowed growth, tissue repair, and clonal (asexual) reproduction.

Stages of Mitosis



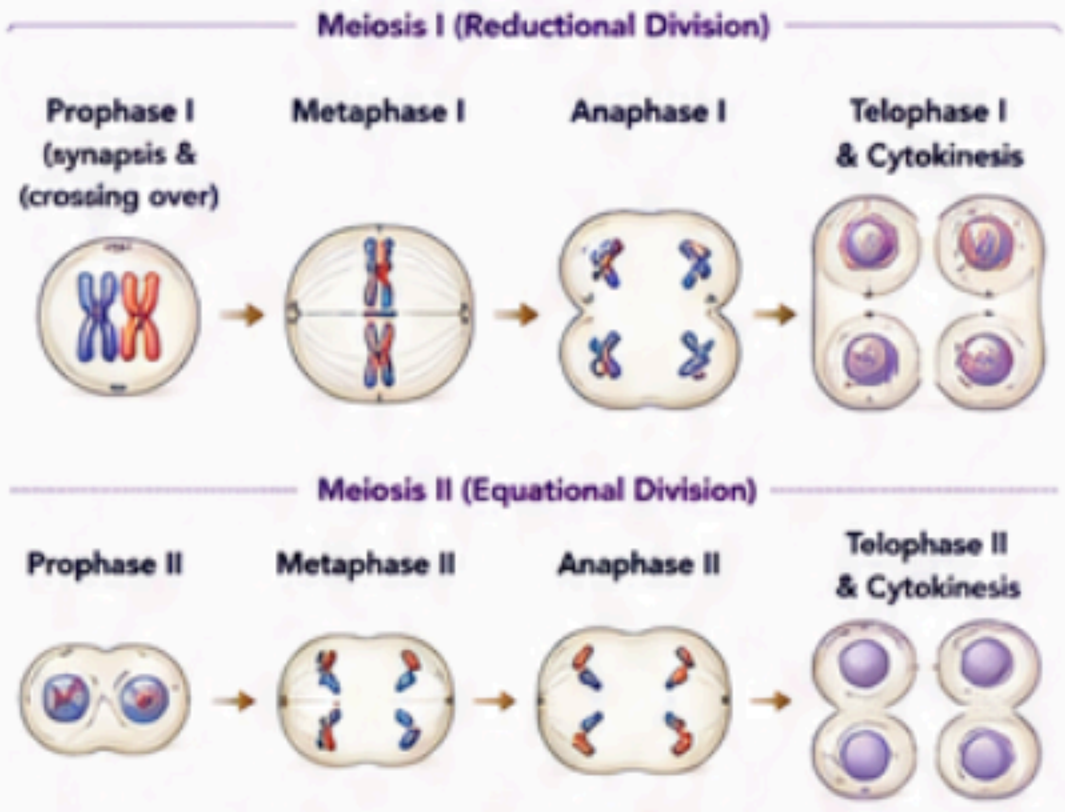
Outcome: Two genetically identical diploid daughter cells.

3. HOW MEIOSIS EVOLVED

As early eukaryotes diversified, sexual reproduction provided new advantages.

- Meiosis evolved as a specialized division to produce gametes with half the chromosome number.
- Likely evolved from a form of mitosis with an additional reduction division.
- Synaptonemal complex and recombination machinery evolved to promote genetic diversity.

Stages of Meiosis


Meiosis I (Reductional Division)
Prophase I (synapsis & (crossing over)
Metaphase I
Anaphase I
Telophase I & Cytokinesis
Meiosis II (Equational Division)
Prophase II
Metaphase II
Anaphase II
Telophase II & Cytokinesis

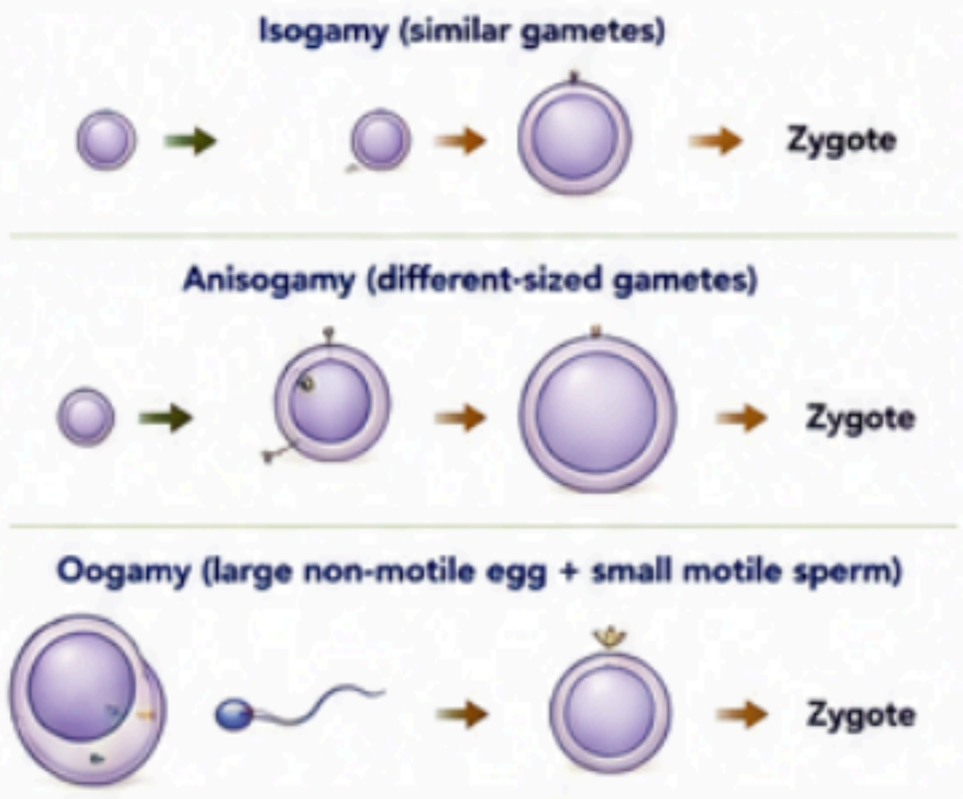
Outcome: Four genetically non-identical haploid gametes.

4. EVOLUTION OF SEXUAL REPRODUCTION

Sexual reproduction likely evolved in steps:

1. Release of haploid cells (gametes) into environment.
2. Fusion of gametes → restores diploidy.
3. Fusion initially may have been random (isogamy).
4. Later evolution of anisogamy (different-sized gametes).
5. Development of mating types and complex behaviors.

Types of Sexual Reproduction (Evolutionary Pathway)


Isogamy (similar gametes)
Zygote
Anisogamy (different-sized gametes)
Zygote
Oogamy (large non-motile egg + small motile sperm)
Zygote

Outcome: Genetic recombination, new gene combinations, and adaptability.

5. HOW DIPLOIDY AND MEIOSIS PROVIDE SURVIVAL ADVANTAGES

A. ADVANTAGES OF DIPLOIDY (2n)

- ☑ **Masking of deleterious mutations:** Recessive harmful mutations are masked by functional alleles.
- ☑ **Gene redundancy:** Extra copies allow one gene to acquire new functions (neofunctionalization).
- ☑ **Increased genetic robustness:** Diploids better withstand environmental stresses and DNA damage.
- ☑ **Facilitates evolution:** Provides raw material for evolution through mutations and gene duplicates.

B. ADVANTAGES OF MEIOSIS

- ☑ **Generates haploid gametes:** Maintains constant chromosome number across generations.
- ☑ **Creates genetic diversity:** Crossing over and independent assortment produce new allele combinations.
- ☑ **Helps remove harmful mutations:** Recombination can separate harmful alleles from beneficial ones.
- ☑ **Drives adaptation:** New combinations increase chance of survival in changing environments.

C. COMBINED POWER: DIPLOIDY + MEIOSIS + FERTILIZATION

- ☑ Sexual cycle allows both stability and variation.
- ☑ Diploid phase preserves successful gene combinations.
- ☑ Meiosis reshuffles genes to create diversity.
- ☑ Fertilization restores diploidy and combines the best of both parents.
- ☑ This cycle enhances long-term survival and evolutionary potential.

Gametes
Fertilization
Diploid Offspring

6. EVIDENCE SUGGESTION THE EVOLUTIONARY TIMELINE

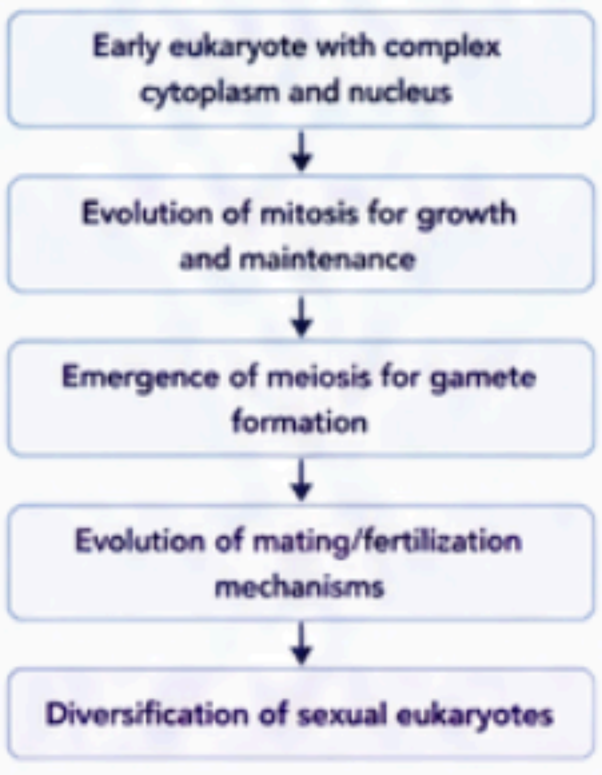
Presence of conserved mitotic proteins (e.g., tubulin, cyclins) across eukaryotes.

Meiosis-specific genes (e.g., SPO11, DMC1) present only in sexual lineages.

Fossil and molecular evidence suggests sexual lineages are ancient.

Many unicellular eukaryotes show both asexual and sexual cycles.

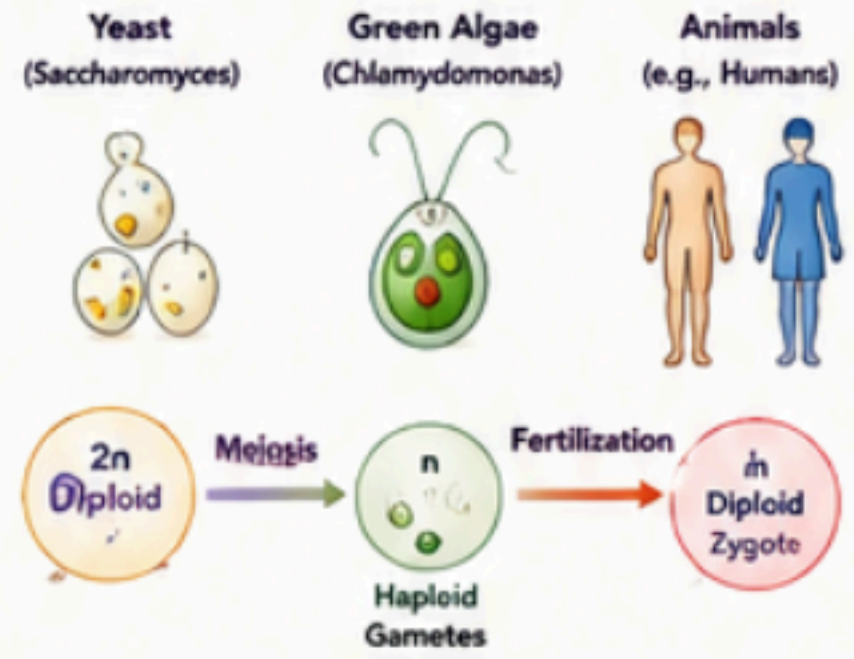
Probable Evolutionary Pathway



Early eukaryote with complex cytoplasm and nucleus
↓
Evolution of mitosis for growth and maintenance
↓
Emergence of meiosis for gamete formation
↓
Evolution of mating/fertilization mechanisms
↓
Diversification of sexual eukaryotes

7. EXAMPLES IN NATURE

Haploid–Diploid (Meiotic) Life Cycles



Demonstrates the universality and success of sexual reproduction in eukaryotes.

8. KEY TAKE-HOME MESSAGES

- ☑ Mitosis evolved to manage complex eukaryotic cells and enable growth and repair.
- ☑ Meiosis evolved as a specialized process to produce gametes and create genetic diversity.
- ☑ Sexual reproduction evolved from simple gamete fusion to complex mating systems.
- ☑ Diploidy provides stability and masks harmful mutations.
- ☑ Meiosis and fertilization generate diversity while maintaining chromosome number.
- ☑ Together, these innovations greatly enhanced the evolutionary success of eukaryotes.

9. SUMMARY COMPARISON

Feature	Mitosis	Meiosis	Sexual Reproduction
Purpose	Growth, repair, asexual reproduction	Gamete formation, variation	Combine genes from two parents
Cell divisions	1	2	Meiosis + Fertilization
Daughter cells	2	4	1 zygote (2n)
Chromosome number	Maintained (2n → 2n)	Reduced (2n → n)	Restored (n + n → 2n)
Genetic variation	None (identical)	High	Very High
Evolutionary role	Cellular success	Diversity generation	Species success

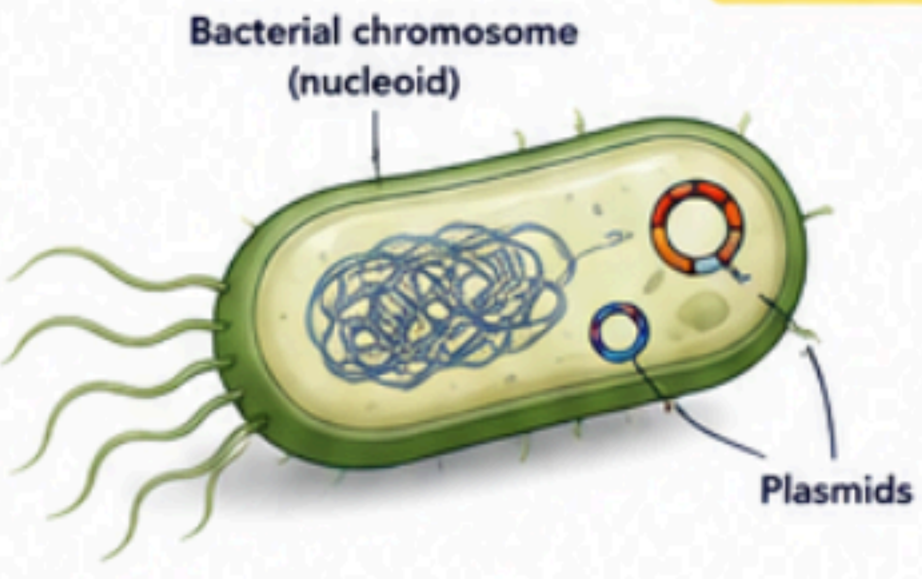
10. CONCLUSION

The evolution of mitosis, meiosis and sexual reproduction represents a series of transformational innovations in early eukaryotes. By combining the stability of diploidy with the diversity generated by meiosis and recombination, sexual reproduction became a powerful engine of evolution—enabling eukaryotic life to adapt, diversify and thrive in a changing world.

Mitosis builds life. Meiosis creates diversity. Sex brings it all together!

4. PLASMIDS AND HORIZONTAL GENE TRANSFER IN BACTERIA

MOBILE DNA THAT DRIVES DIVERSITY, ADAPTATION AND EVOLUTION



PLASMIDS are extrachromosomal, usually circular, double-stranded DNA molecules that replicate independently of the bacterial chromosome.

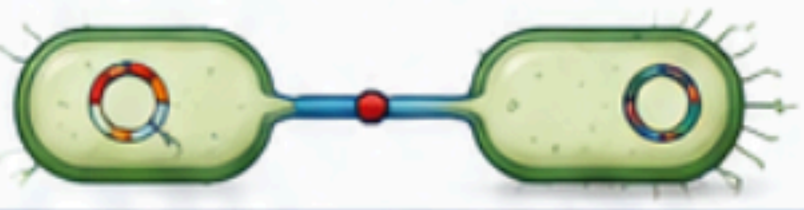
Key Features

- Small (1 kb to >200 kb)
- Self-replicating (have origin of replication, *ori*)
- Often carry accessory genes beneficial for survival
- May be transferable between bacteria
- Can exist in multiple copies per cell
- Encode genes for resistance, virulence, metabolism, etc.

HORIZONTAL GENE TRANSFER (HGT)

Transfer of genetic material between organisms other than through vertical inheritance.

Plasmids are major agents of HGT via **CONJUGATION** (cell-to-cell transfer).

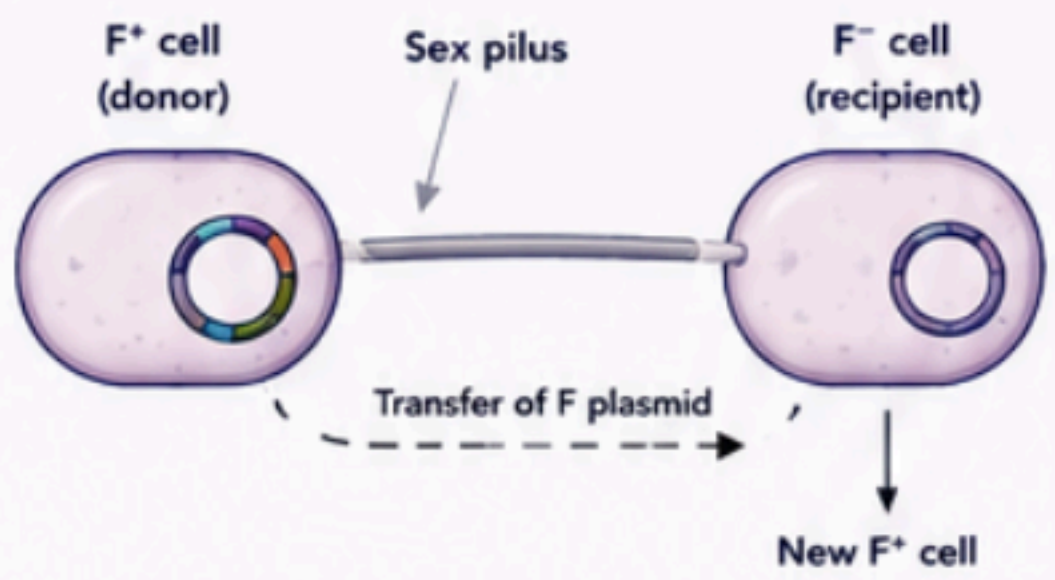


Other HGT mechanisms: Transformation, Transduction, Conjugation (plasmid-mediated)

TYPES OF F-RELATED PLASMIDS AND THEIR ROLE IN CONJUGATION

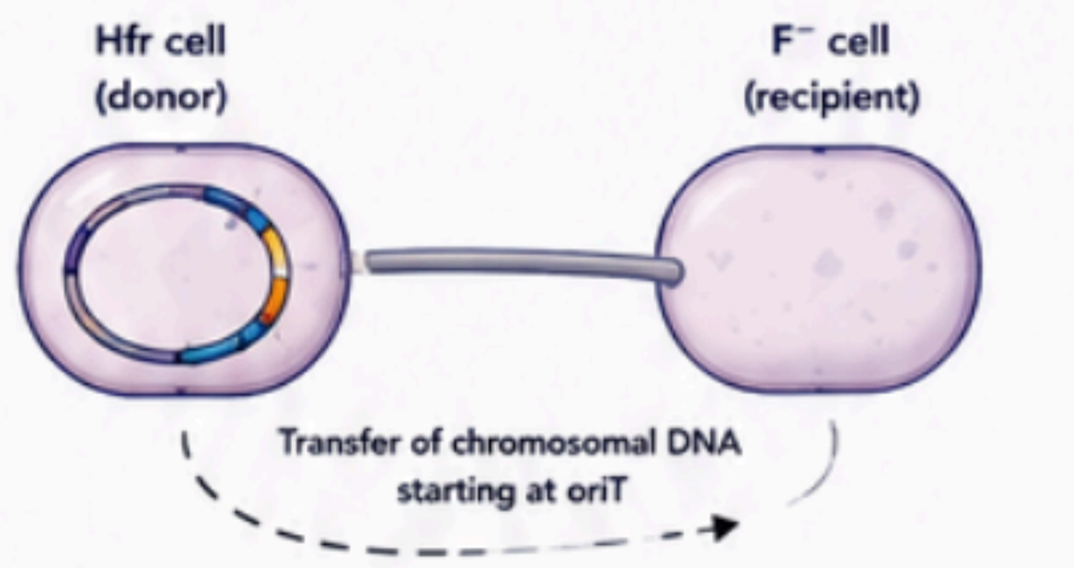
① F (Fertility) PLASMID

- Small (~100 kb) conjugative plasmid.
- Carries *tra* (transfer) genes and *oriT* (origin of transfer).
- Encodes sex pilus for mating bridge formation.
- Transfers itself from F^+ (donor) to F^- (recipient) cell.
- Recipient becomes F^+ after acquiring F plasmid.



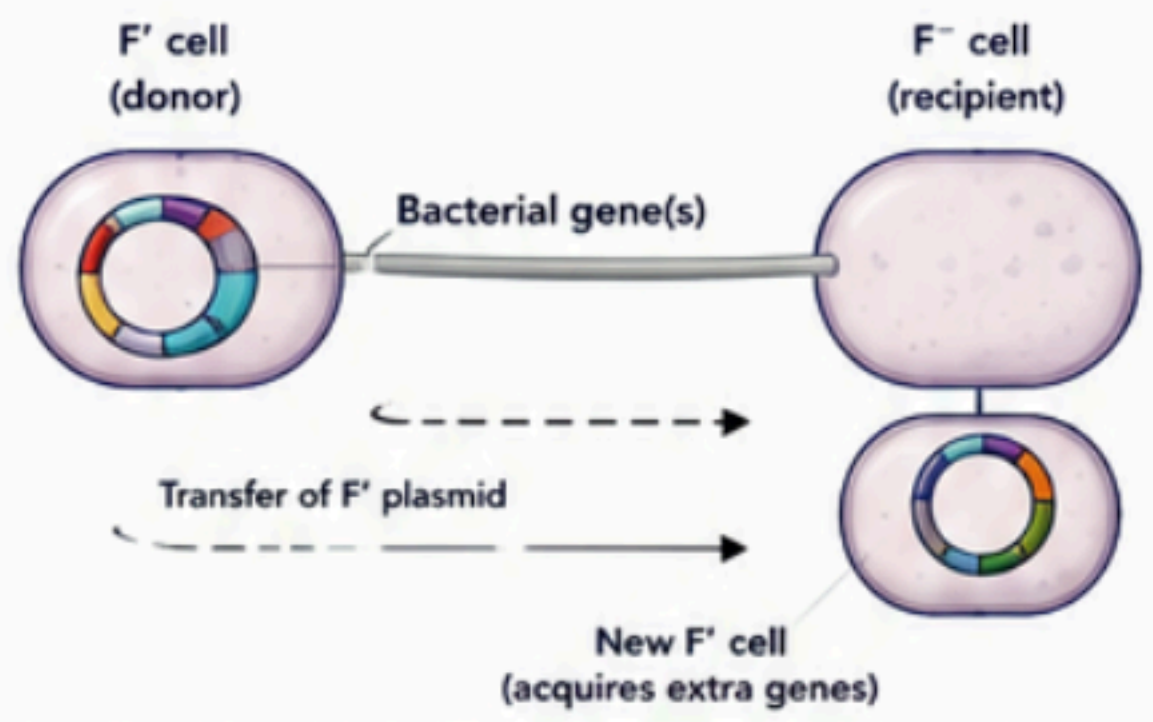
② Hfr (High Frequency of Recombination) PLASMID

- F plasmid integrates into the bacterial chromosome by homologous recombination.
- Integrated plasmid is called Hfr (F integrated) strain.
- During conjugation, parts of the bacterial chromosome are transferred to recipient (but F plasmid usually does not transfer completely).
- Recipient remains F^- but may acquire new genes via recombination (high frequency).



③ F′ (F-prime) PLASMID

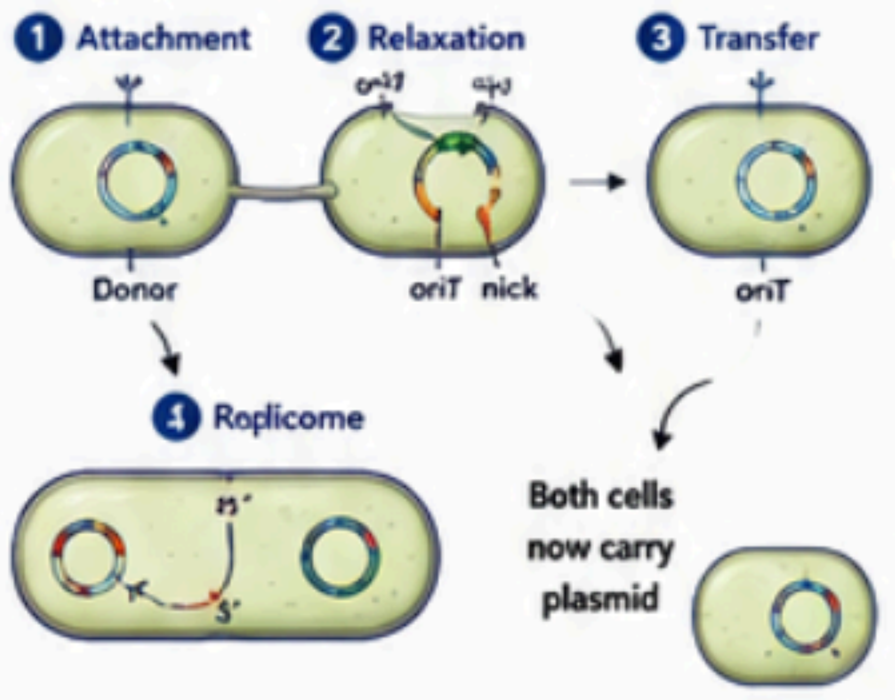
- Rare excision of the integrated F plasmid with adjacent bacterial genes.
- Forms an F′ plasmid (carries bacterial genes).
- Transfers to recipient as a plasmid, converting F^- cell to F′.
- Recipient receives both the F plasmid and additional bacterial genes.



ROLE OF PLASMIDS IN HORIZONTAL GENE TRANSFER

How Conjugative Plasmids Work

1. **Attachment:** Donor (F^+, Hfr or F′) attaches to recipient (F^-) via sex pilus.
2. **Relaxation:** Relaxase enzyme nicks *oriT* and unwinds one DNA strand.
3. **Transfer:** Single-stranded DNA is transferred to recipient.
4. **Replication:** Rolling-circle replication in donor; complementary strand synthesized in recipient.
5. **Outcome:** Plasmid (and sometimes chromosomal genes) is maintained in both cells.



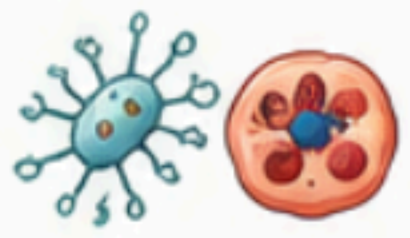
SIGNIFICANCE OF PLASMIDS

Antibiotic Resistance

- Plasmids carry resistance genes (e.g., bla_{TEM}, mecA, ndm-1, tetA, sul_1).
- Enable survival in presence of antibiotics.
- Often carry multiple resistance genes (multi-drug resistance plasmids).

Virulence

- Plasmids carry virulence genes encoding toxins, adhesins, invasins, secretion systems, etc.
- Convert non-pathogenic bacteria into pathogenic ones.



Genetic Recombination and Diversity

- Facilitate gene exchange between bacteria.
- Promote evolution and adaptation.
- Create new gene combinations and phenotypes.

IMPORTANT PLASMID-BORNE ELEMENTS AND EXAMPLES

Element / Plasmid Type	Key Genes / Features	Examples	Role / Importance
R plasmids (Resistance)	Antibiotic resistance genes	pBR322, pUC plasmids	Drug resistance, multidrug resistance
Virulence plasmids	Toxin, adhesin, iron acquisition genes	pXO1 (*B. anthracis*), pYV (*Yersinia pestis*)	Pathogenicity and disease
F plasmid	tra genes, *oriT*, fertility functions	F (fertility factor)	Conjugation, self-transfer
Hfr plasmid	F integrated into chromosome	Hfr strains (e.g., HfrH)	Transfer of chromosomal genes
F′ plasmid	F′ plasmid with host genes	F′ *lac*⁺, F′ met⁺	Transfer of plasmid + host genes
Degradative plasmids	Catabolic pathway genes	NAH7 (naphthalene degradation)	Environmental adaptation
Metabolic plasmids	Metabolic / biosynthetic genes	pSym (Rhizobium)	Nutrient utilization, symbiosis

EXAMPLES OF PLASMID-MEDIATED HGT

- Spread of β-lactamase genes (e.g., $bla_{NOM\text{-}1}$, bla_{KPC}) via plasmids among Enterobacteriaceae.
- Methicillin resistance in *Staphylococcus aureus* via SCCmec (a mobile genetic element on plasmid).
- Toxin genes in *Vibrio cholerae* (*ctxAB* on filamentous phage but maintenance aided by plasmid factors).
- Virulence plasmid in *Agrobacterium tumefaciens* (causes crown gall in plants).

BIOLOGICAL IMPACT

- ☑ Enhances survival under antibiotic pressure.
- ☑ Allows rapid acquisition of new functions.
- ☑ Facilitates colonization of new niches.
- ☑ Increases bacterial fitness and competitiveness.
- ☑ Major driver of antimicrobial resistance (AMR) crisis.

WHY F, Hfr AND F′ MATTER?

- **F plasmid:** spreads plasmids and maintains conjugation.
- **Hfr plasmid:** transfers chromosomal genes → genetic diversity.
- **F′ plasmid:** transfers plasmid + host genes → stable inheritance.

Together, they are powerful tools of genetic exchange and evolution.

KEY TAKE-HOME MESSAGES

- ☑ Plasmids are mobile genetic elements central to HGT.
- ☑ F, Hfr and F′ plasmids mediate gene transfer by conjugation.
- ☑ They carry genes for antibiotic resistance, virulence and adaptation.
- ☑ Plasmid-mediated HGT accelerates evolution and poses public health challenges but is also exploited in biotechnology.

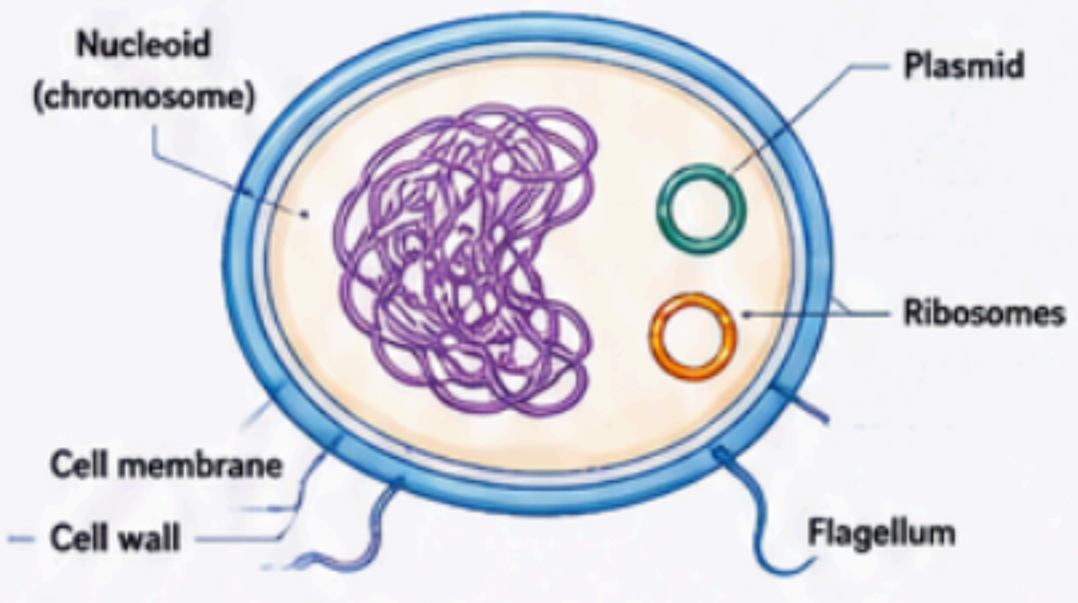
PLASMIDS: SMALL DNA, BIG IMPACT!

Drivers of horizontal gene transfer, adaptation, pathogenesis and evolution in bacteria.

③ BACTERIAL GENOMES

KEY FEATURES, VARIABILITY AND BIOLOGICAL SIGNIFICANCE

1. KEY FEATURES OF BACTERIAL GENOMES



- Usually a single, circular, double-stranded DNA molecule located in the nucleoid (haploid).
- Size varies widely: ~0.5 Mbp (*Mycoplasma genitalium*) to >10 Mbp (*Streptomyces coelicolor*).
- High gene density: ~85–95% of DNA codes for proteins (less non-coding DNA).
- Operons common: genes for related functions are co-regulated.
- Plasmids: extra-chromosomal DNA, often carrying accessory or adaptive genes.
- Mobile genetic elements (IS elements, transposons, phages) contribute to genome plasticity.
- Typically lack histones (except some actinomycetes-like proteins). Supercoiled DNA helps compact the genome.

2. GENOMIC VARIABILITY IN BACTERIA

Sources of Variability

Mutation
Point mutations, insertions, deletions, and genome rearrangements create new variants.

Horizontal Gene Transfer (HGT)
Transformation, transduction and conjugation introduce new genes.

Gene Duplication
Creates redundant genes that may evolve new functions.

Mobile Genetic Elements
Transposons, insertion sequences, integrons and phages drive genome change.

Recombination & Gene Conversion
Exchange of DNA segments introduces diversity.

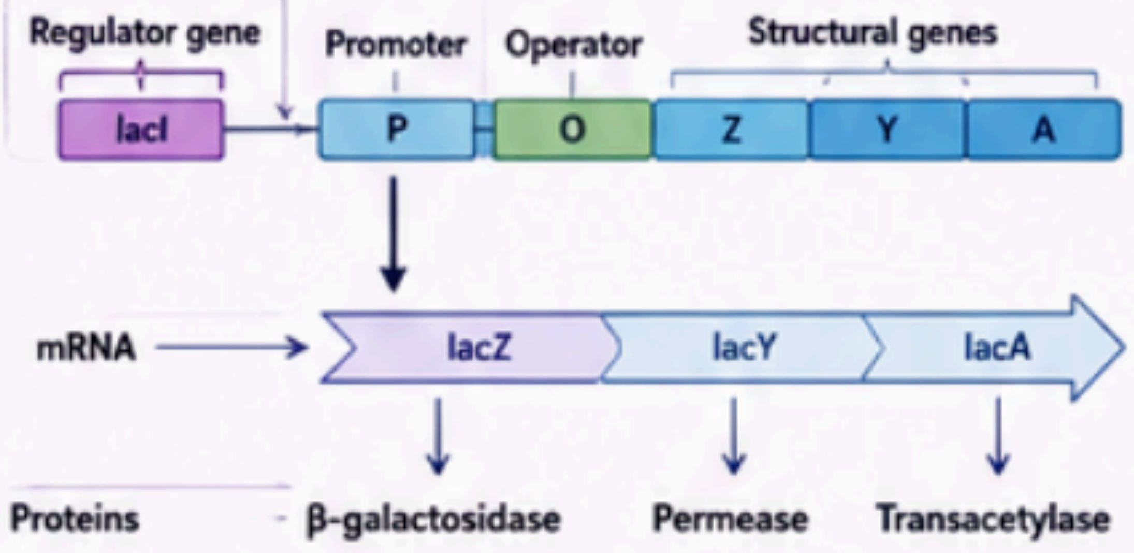
Outcomes of Variability

- Antibiotic resistance
- Metabolic versatility
- Virulence and host adaptation
- Environmental adaptation
- Speciation and evolution

3. OPERONS – COORDINATED GENE EXPRESSION

Definition: A cluster of genes under the control of a single promoter, transcribed together as a polycistronic mRNA.

Typical Structure (e.g., lac operon)



Key Points
- Ensures efficient use of resources.
- Allows coordinated expression of functionally related genes.
- Regulation can be inducible (e.g., *lac*), repressible (e.g., *trp*) or catabolite-repressed (e.g., *ara*).

4. PLASMIDS – EXTRACHROMOSOMAL ELEMENTS

Small, circular DNA molecules that replicate independently of the chromosome.

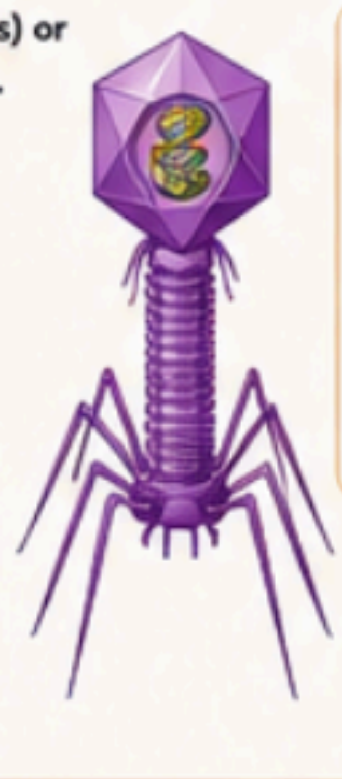
Functions
- Carry accessory genes (antibiotic resistance, virulence, metabolic pathways).
- Conjugative plasmids have genes for transfer.
- Copy number varies (low or high).

Examples: R-plasmids (resistance), Ti plasmid (*Agrobacterium*), Col plasmids (*E. coli*).

5. PHX GENES (PROPHAGE-ASSOCIATED OR PHAGE HYPOTHETICAL GENES)

PHX genes are found in bacteriophages (phage genomes) or prophage regions integrated into bacterial chromosomes.

Key Features
- Encode hypothetical proteins with unknown or predicted functions.
- Many are involved in phage replication, host interaction, lysogeny, virulence, immunity or DNA metabolism.
- Some contribute to bacterial fitness, stress response, or pathogenicity (e.g., toxins, superantigens).
- Act as a reservoir of novel genes for evolution via horizontal transfer.



Roles/Significance
- Influence bacterial evolution and adaptation.
- Mediate lysogenic conversion (e.g., toxin production in *Corynebacterium diphtherioe*).
- Source of new metabolic or regulatory genes.
- Important in biotechnology (vectors, gene therapy, phage display).

PHX genes highlight the intimate link between phages and bacterial genome diversification.

6. ADAPTATIONS IN DEINOCOCCUS RADIODURANS

Deinococcus radiodurans is one of the most organisms known.

Key Adaptations

Extraordinary DNA Repair
- Multiple copies of genes for repair proteins.
- Efficient systems for double-strand break repair via homologous recombination.

Protective Enzymes
- High levels of Mn^{2+} (replaces Fe^{2+}) protect proteins from oxidative damage.
- Strong antioxidant enzymes (catalase, superoxide dismutase).

Unique Chromosome Structure
- Genome organized in a compact nucleoide with DNA-binding proteins (Dps-like) that protect DNA.

Efficient Damage Tolerance
- Can survive doses >5,000 Gy of radiation.
- Reassembles shattered genome accurately.

Pigmentation & Membrane Protection
- Carotenoids scavenge free radicals.
- Robust cell envelope protects from UV and desiccation.

These adaptations make *D. radiodurans* a model for extreme stress resistance and astrobiology studies.

7. BIOLOGICAL SIGNIFICANCE OF BACTERIAL GENOMES

Survival & Adaptation

Enable rapid adaptation to diverse environments through genetic flexibility.

Pathogenicity

Presence of virulence genes, toxins, secretion systems and antibiotic resistance genes.

Biotechnology

Source of enzymes, metabolic pathways, and genetic tools (plasmids, vectors).

Ecological Roles

Drive nutrient cycling, symbiosis, and bioremediation in ecosystems.

Evolutionary Insight

Help trace evolutionary relationships and gene flow across populations.

8. SUMMARY TABLE

Component	Description	Role / Significance	Example
Chromosome	Main circular DNA in nucleoid	Carries essential genes for survival	*E. coli* (4.6 Mbp)
Operons	Cluster of co-regulated genes	Coordinate expression of related functions	*lac, trp, ara* operons
Plasmids	Extra-chromosomal DNA	Carry accessory genes (adaptetion)	R-plasmid (resistance)
PHX Genes	Phage or prophage-associated genes	Influence evolution, virulence, adaptation	Toxin genes in *C. diphtherioe*
Variability	Mutations, HGT, recombination	Generates diversity and new traits	Antibiotic resistance
D. radiodurans Adaptations	DNA repair, antioxidants, Mn^{2+}, pigments	Extreme resistance to radiation and stress	Survives >5,000 Gy

9. KEY TAKE-HOME MESSAGES

- ☑ Bacterial genomes are compact, dynamic and highly adaptable.
- ☑ Operons ensure efficient, coordinated gene expression.
- ☑ Plasmids and PHX genes drive genetic diversity and evolution.
- ☑ Variability enables rapid adaptation to environments and selective pressures.
- ☑ *D. radiodurans* demonstrates how genome organization and protective mechanisms confer extreme stress resistance.

Bacterial genomes are remarkable for their economy, flexibility and innovation—the foundation of bacterial success in every habitat on Earth.

2. PHYLOGENETIC TREES

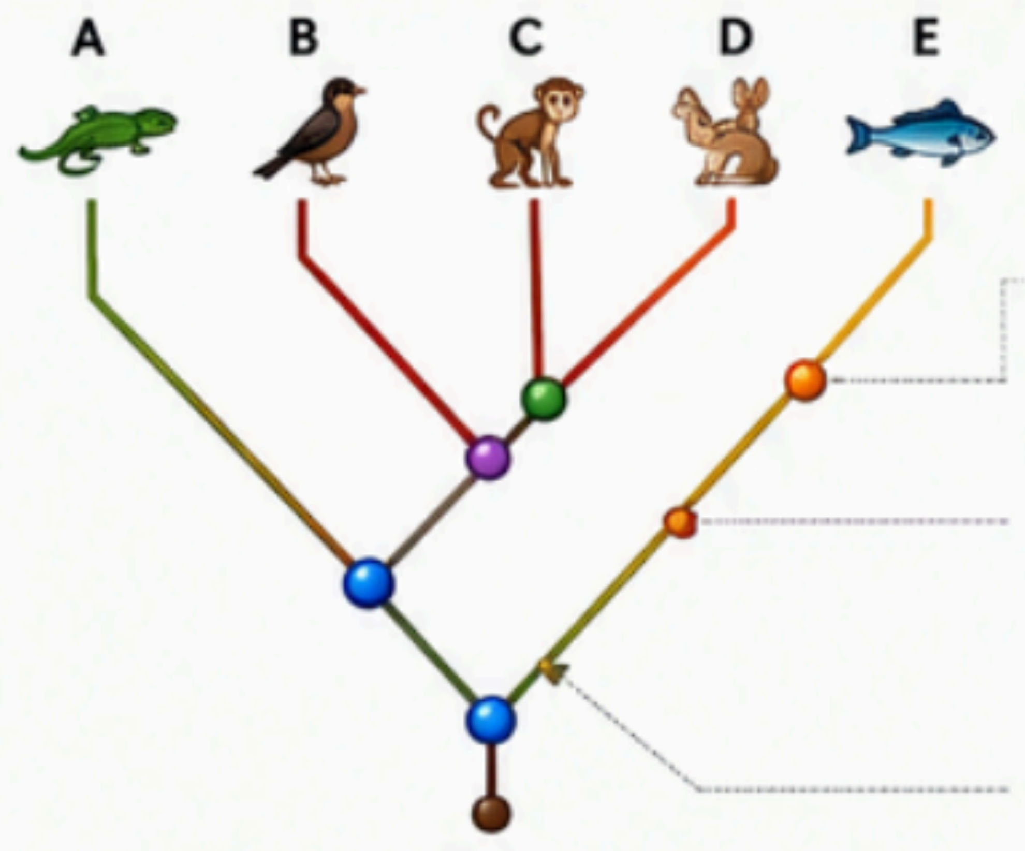
A map of evolutionary relationships

Phylogenetic trees (or phylogenies) are diagrams that show the evolutionary relationships among organisms or genes based on shared ancestry.

KEY IDEA

They do not show how organisms look or behave, but how they are related through evolution.

1. KEY FEATURES OF PHYLOGENETIC TREES



Root
The common ancestor of all taxa in the tree.

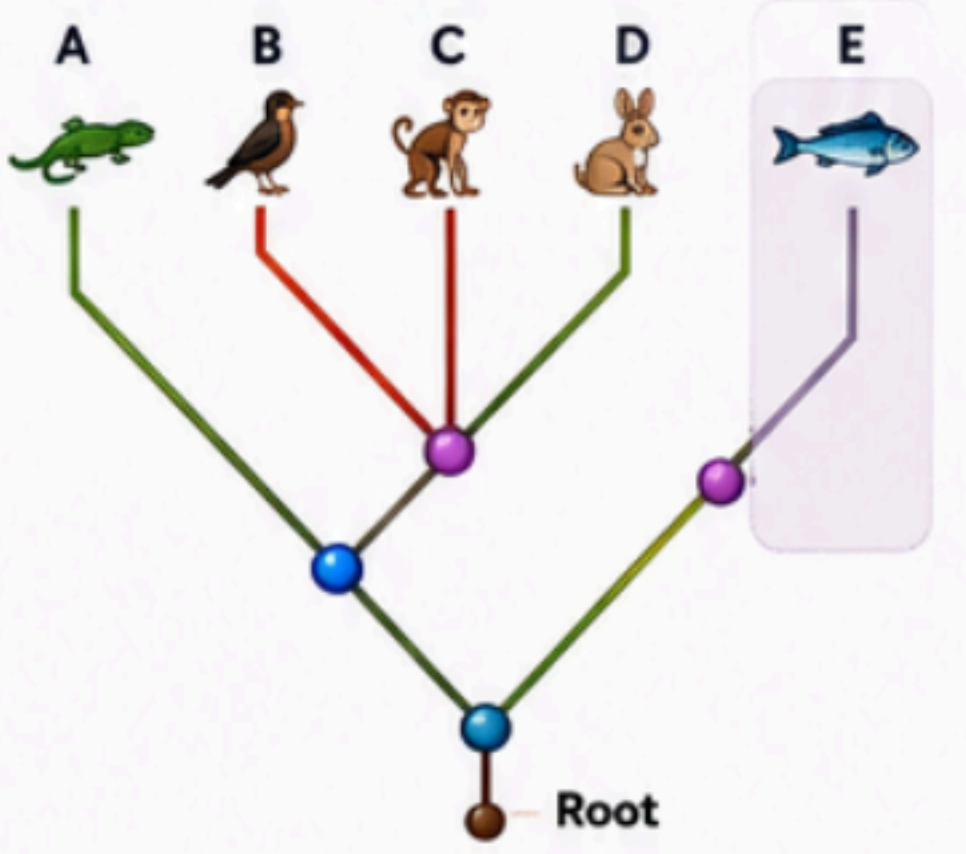
Terminal nodes (tips)
Represent the observed taxa (species, genes, etc.).

Branches
Represent evolutionary lineages.

Nodes
Points where branches split. They represent common ancestors.

Internal nodes
Represent ancestors that are not observed (hypothetical ancestors).

2. ROOT, OUTGROUP AND DIRECTION

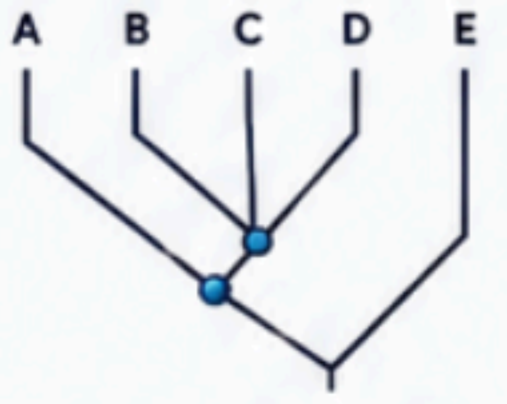


- **Root:** The base of the tree. It represents the most recent common ancestor of all taxa in the tree.
- **Outgroup (E):** A taxon known to be outside the group of interest. It is used to root the tree and determine the direction of evolution.
- **Direction of evolution:** Evolutionary changes are inferred from the root toward the tips.

Example: E is the outgroup. It helps us infer that A, B, C and D share a more recent common ancestor with each other than with E.

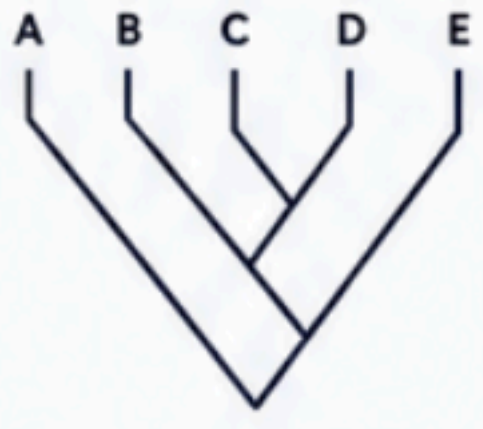
3. SCALED (PHYLOGRAM) vs UNSCALED (CLADOGRAM)

Phylogram (scaled tree)



- Branch lengths are proportional to the amount of evolutionary change (e.g., genetic change or time).
- Used to show how much change has occurred.

Cladogram (unscaled tree)

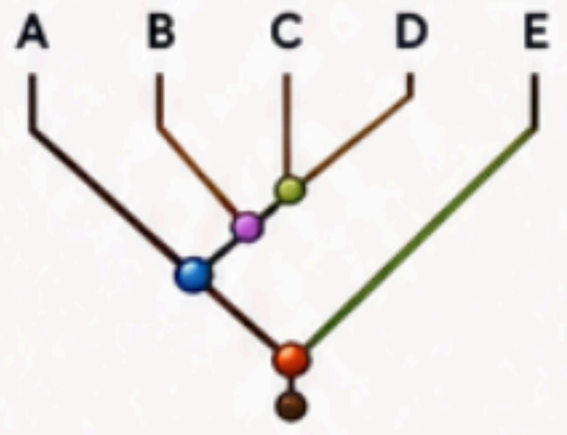


- Branch lengths are not proportional to change.
- Only the branching order (topology) is meaningful.

Both trees show the same relationships, but phylograms include information about the amount of change.

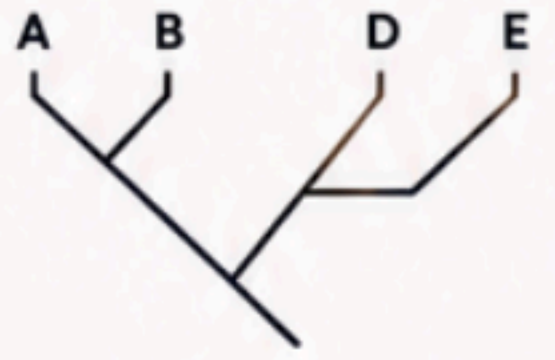
4. ROOTED vs UNROOTED TREES

Rooted tree



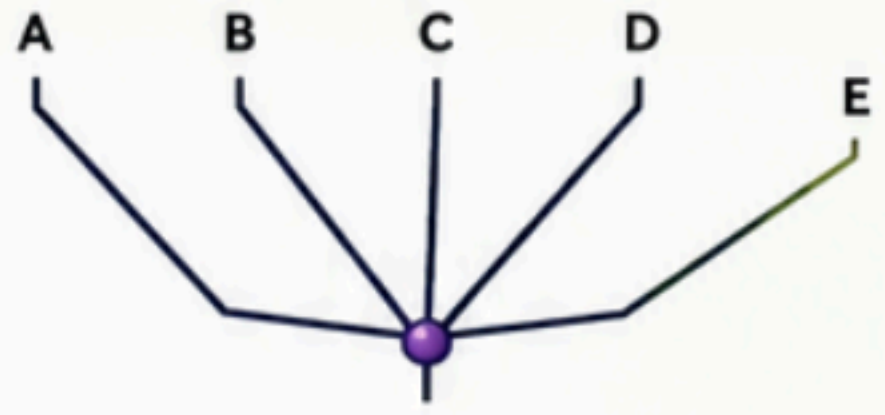
- Has a root.
- Shows the direction of evolution from ancestor (root) to descendants (tips).

Unrooted tree



- No root.
- Shows relationships but not the direction of evolution.

5. POLYTOMY



A polytomy occurs when a node splits into more than two descendant lineages.

Reasons:

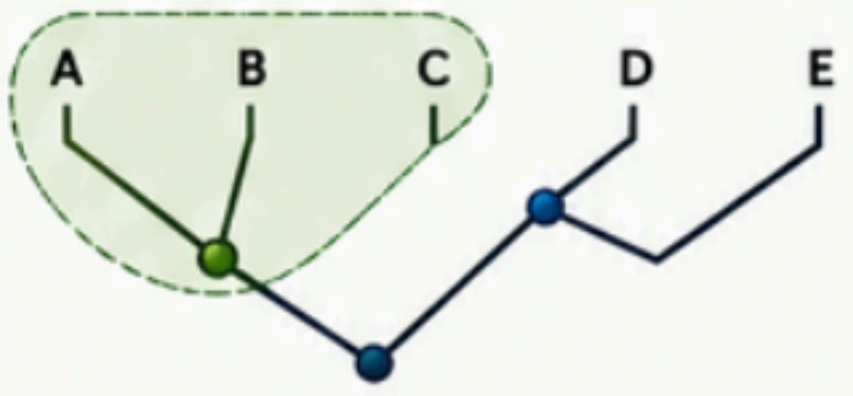
- Rapid radiation (many lineages evolved quickly).
- Insufficient data to resolve relationships.
- True simultaneous divergence.

Polytomies indicate uncertainty or unresolved relationships.

6. TYPES OF GROUPS IN PHYLOGEENETIC TREES

1. MONOPHYLETIC (CLADE)

Includes a common ancestor and ALL of its descendants.

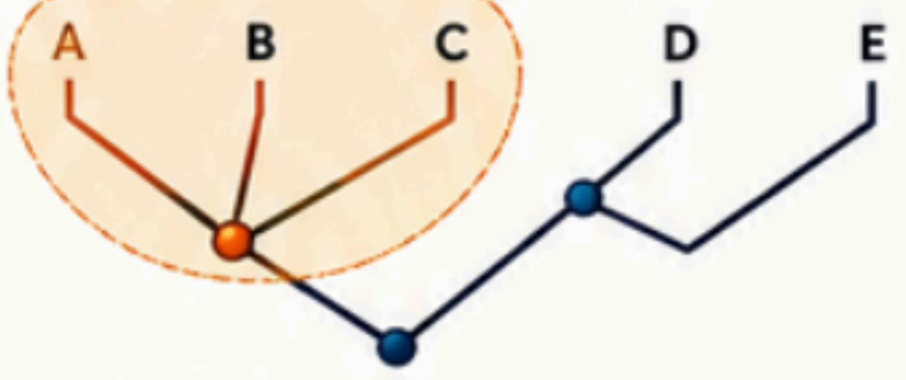


Example: Group {A, B, C} is monophyletic because it includes their common ancestor and all descendants.

These groups reflect natural evolutionary units.

2. PARAPHYLETIC GROUP

Includes a common ancestor but NOT all of its descendants.

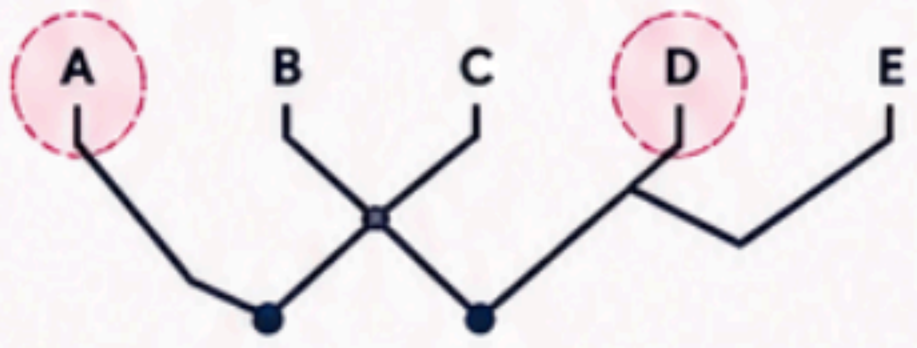


Example: Group {A, B, C} is paraphyletic if D is also a descendant of their common ancestor but is excluded.

Traditional groups like "reptiles" (excluding birds) are paraphyletic.

3. POLYPHYLETIC GROUP

Includes members from different lineages without their most recent common ancestor.



Example: Group {A, D} is polyphyletic because they do not share an immediate common ancestor within the group.

These groups are artificial and do not reflect evolution.

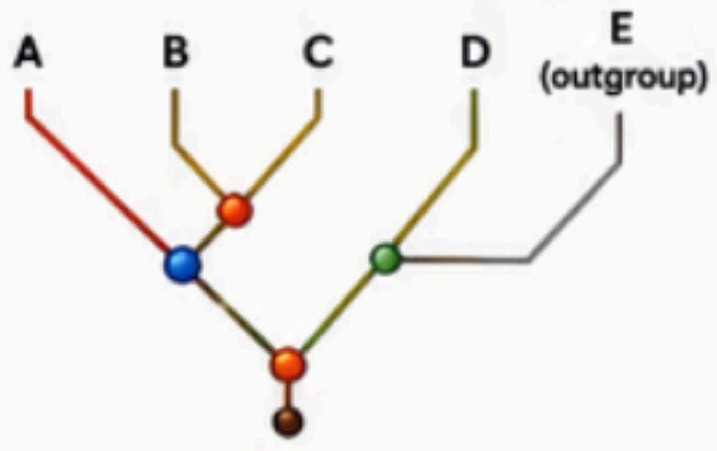
QUICK REFERENCE: TERMS

●	Root	The base of a rooted tree; common ancestor of all taxa.
●	Outgroup	A taxon outside the group of interest used to root the tree.
●	Node	A branching point representing a common ancestor.
●	Terminal node (tip)	An observed taxon at the end of a branch.
●	Branch	A lineage connecting nodes (ancestors and descendants).
●	Internal node	A hypothetical ancestor not directly observed.
●	Polytomy	A node with more than two descendant branches.

HOW TO READ A PHYLOGENETIC TREE

- ✓ Find the root (if present).
- ✓ Identify how taxa are related by tracing back to common ancestors (nodes).
- ✓ Tips that share a more recent common ancestor are more closely related.
- ✓ Branch length matters only in phylograms, not in cladograms.
- ✓ Use the outgroup to infer the direction of evolution.

EXAMPLE SUMMARY



- E roots the tree.
- A and B are sister taxa.
- C is more closely related to (A,B) than to D or E.
- D is more distant from A, B, and C.

This tree is rooted, unscaled (cladogram), and shows a monophyletic group (A, B, C).

REMEMBER

Phylogenetic trees are powerful tools for showing evolutionary history. Understanding their features helps us interpret the tree correctly and draw meaningful biological conclusions.

APPLICATIONS

- Understanding evolution and biodiversity
- Classification of organisms
- Tracking disease evolution (e.g., viruses)
- Conservation biology

1. (a) EVOLUTION EXPLAINS ANTIBIOTIC RESISTANCE

How the principles of evolutionary biology account for antibiotic resistance

Antibiotic resistance is not a new ability acquired by bacteria "on purpose". It is the outcome of evolution—heritable variation + natural selection acting on bacterial populations.

EVOLUTIONARY PRINCIPLES AT WORK

1 GENETIC VARIATION

Random mutations and gene combinations create differences among bacteria. Some variations may reduce the effect of an antibiotic.

2 HERITABILITY

Helpful variations (e.g., resistance genes) are heritable and passed on to daughter cells and future generations.

3 OVERPRODUCTION

Bacteria reproduce rapidly. Huge populations mean even rare resistant variants are likely to exist.

4 NATURAL SELECTION

Antibiotics kill susceptible bacteria but resistant ones survive.

5 ADAPTATION OF POPULATION

Resistant bacteria multiply and become the majority. The population evolves.

HOW ANTIBIOTIC RESISTANCE EVOLVES: STEP-BY-STEP

1 Variation arises
In a large population, random mutations or gene acquisition (some bacteria have resistance genes; most do not).

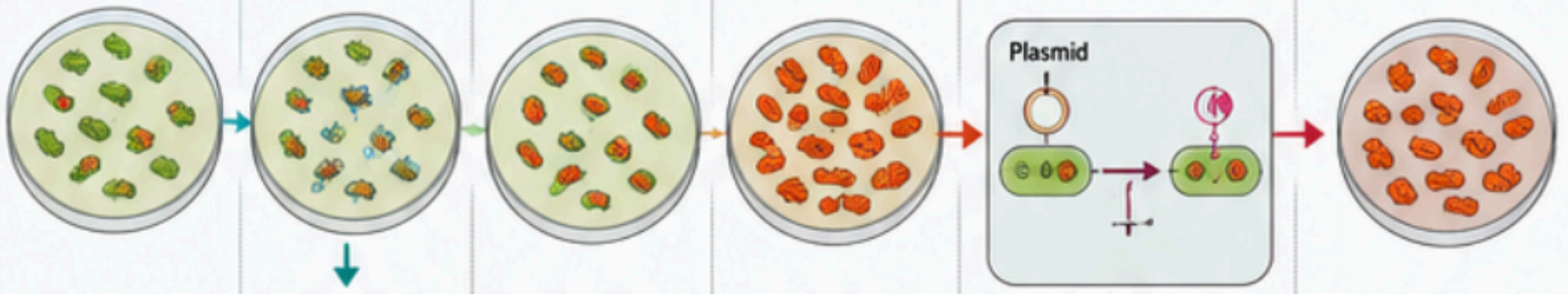
2 Antibiotic is used
The antibiotic creates environmental pressure by killing susceptible bacteria.

3 Survivors remain
Resistant bacteria survive because the antibiotic cannot kill them effectively.

4 Reproduction
Survivors multiply rapidly and pass on resistance to their offspring.

5 Spread of resistance genes
Resistance genes can spread to other bacteria through horizontal gene transfer (HGT).

6 Resistant population dominates
Over time, most bacteria in the population are resistant. The antibiotic becomes ineffective.



ANTIBIOTIC PRESENT

RESISTANT ONES SURVIVE

POPULATION GROWS

CONJUGATION (pilus)

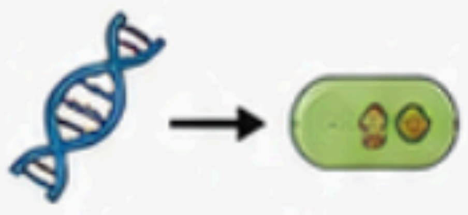
RESISTANCE DOMINATES

This is evolution in action: variation → selection → differential survival → inheritance → change in population.

WAYS BACTERIA BECOME RESISTANT

1. MUTATION

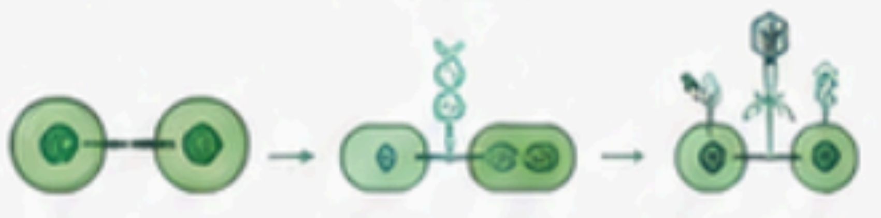
Changes in DNA may alter target sites, reduce drug uptake or increase efflux of the antibiotic.



e.g., mutation in gene for target protein

2. HORIZONTAL GENE TRANSFER (HGT)

Bacteria share resistance genes with other bacteria.



Conjugation (cell-to-cell transfer)

Transformation (uptake of free DNA)

Transduction (virus/phage transfer)

HGT allows rapid spread, even across species.

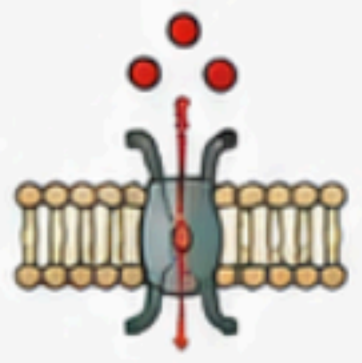
3. ENZYMATIC DEGRADATION

Bacteria produce enzymes (e.g., β-lactamases) that break down antibiotics.

e.g., breaks the antibiotic molecule

4. EFFLUX PUMPS & DECREASED UPTAKE

Bacteria pump out the drug or reduce entry.



EXAMPLES OF EVOLUTION IN REAL LIFE

- **MRSA** (Methicillin-resistant Staphylococcus aureus) — evolved resistance to methicillin and many other drugs.
- **XDR-TB** (Extensively Drug-Resistant Tuberculosis) — evolved against multiple anti-TB drugs.
- **Carbapenem-resistant Enterobacteriaceae (CRE)** — evolved resistance to last-resort antibiotics.
- **Malaria** parasites evolving resistance to antimalarial drugs.

BROADER APPLICATIONS IN SCIENCE AND SOCIETY

1 MEDICINE & PUBLIC HEALTH

- Understands emergence and spread of resistance in hospitals and communities.
- Guides treatment choices and antibiotic stewardship programs.
- Informs vaccine development (evolutionary arms race approach).
- Helps in outbreak investigation and infection control.

2 MICROBIOLOGY & RESEARCH

- Studies mechanisms of resistance (genes, mutations, HGT).
- Develops new antibiotics and adjuvant therapies (e.g., enzyme inhibitors).
- Uses evolutionary experiments in labs to predict resistance pathways.

3 EVOLUTIONARY BIOLOGY

- A real-time example of natural selection in action.
- Shows microevolution leading to rapid adaptive change.
- Helps understand coevolution (host-pathogen-drug dynamics).
- Provides case studies for teaching evolution.

4. AGRICULTURE & VETERINARY SCIENCE

- Overuse of antibiotics in livestock selects for resistant bacteria.
- Resistant bacteria can spread to humans via food, water, soil, or direct contact.
- Promotes responsible use of antibiotics in animal husbandry and aquaculture.

5. ENVIRONMENT & ECOLOGY

- Antibiotics in wastewater and soil create selective pressure.
- Environmental reservoirs of resistance genes (resistome) can spread to human pathogens.
- Supports policies for reducing pharmaceutical pollution.

6. BIOTECHNOLOGY & INDUSTRY

- Engineer bacteriophages and probiotics to combat infections.
- Develop rapid diagnostic tools to detect resistance genes.
- Biotech innovations for novel drug targets and alternative therapies.

THE SOCIETAL IMPACT

- Longer illnesses and higher treatment costs
- Increased deaths from common infections
- Threatens surgeries, cancer therapy, organ transplants
- Economic burden on healthcare systems
- Widening health inequalities globally

WHAT CAN WE DO?

- ✓ Use antibiotics only when prescribed.
- ✓ Complete the full course as directed.
- ✓ Never use leftover or someone else's antibiotics.
- ✓ Prevent infections: hygiene, vaccination, clean water.
- ✓ Improve surveillance and rapid diagnostics.
- ✓ Invest in research for new drugs and alternatives.
- ✓ Promote **One Health** approach: humans, animals, environment together.

KEY TAKEAWAYS

- ✓ Antibiotic resistance is an evolutionary response to selective pressure.
- ✓ It arises from natural genetic variation, not from need or intention.
- ✓ Misuse and overuse of antibiotics speed up evolution.
- ✓ Understanding evolution helps us predict, prevent and manage resistance.
- ✓ Responsible action today protects the effectiveness of antibiotics for tomorrow.

> "We do not inherit the Earth
> from our ancestors;
> we borrow it from
> our children."
>
> — Native American Proverb

EVOLUTION CANNOT BE STOPPED, BUT ITS DIRECTION CAN BE INFLUENCED BY OUR CHOICES.
USE RESPONSIBLY. PRESERVE EFFECTIVENESS. PROTECT FUTURE.

(b)

FROM THE BIG BANG TO LIFE ON EARTH

How the Big Bang theory, formation of Earth, and chemical evolution together explain the origin of life on our planet.

Life did not appear suddenly. It emerged through a series of natural processes operating over billions of years.
The Big Bang created the universe and the elements. Earth formed in this universe.
On early Earth, simple chemicals formed complex molecules, which organized into systems capable of life.

1 THE BIG BANG: THE START OF EVERYTHING

13.8 billion years ago

The Big Bang

The universe begins as an extremely hot, dense point.

10^{-6} seconds

Particles form

Quarks form protons and neutrons; electrons exist in a hot soup.

3 minutes

Light elements

Big Bang nucleosynthesis produces H, He, and trace Li.

380,000 years

Atoms & light

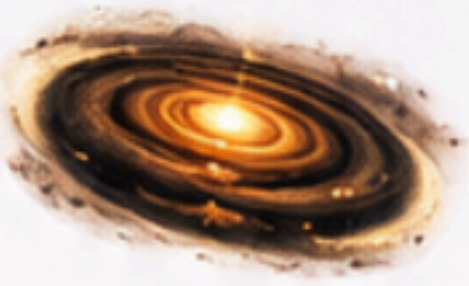
Electrons combine with nuclei; light is released (Cosmic Microwave Background).

100 million–1 billion years

Stars & galaxies

Gravity gathers matter into stars and galaxies. Inside stars, heavier elements (C, N, O, P, S, Fe, etc.) are made.

4.6 billion years ago



Solar system forms

A cloud of gas and dust collapses to form the Sun and a protoplanetary disk. Planets, asteroids and comets form.

KEY TAKEAWAYS

- The Big Bang explains the origin of space, time, matter and energy.
- Elements essential for life were created in the universe.
- Earth is made of star-stuff—material forged in ancient stars.

2 FORMATION OF EARTH: A HABITABLE WORLD EMERGES

4.6 billion years ago

Accretion

Dust and rock in the solar nebula collide and stick together, forming Earth. Early Earth is hot and heavily bombarded.

4.5–4.4 billion years ago

Differentiation & Cooling

Earth separates into layers (core, mantle, crust). Surface cools and a solid crust forms.

4.4–4.3 billion years ago

Water & Oceans

Water vapor form volcanoes and icy bodies condenses, forming oceans.

4.1–3.8 billion years ago

Early Atmosphere

Composed of gases like CO_2, N_2, H_2O, CH_4, NH_3, H_2, CO. No free oxygen.

Energy Sources Abundant on Early Earth

- Lightning
- Ultraviolet sunlight
- Volcanic heat
- Hydrothermal vents
- Impact energy

A Stable Environment for Chemistry

- Oceans dissolve and concentrate chemicals
- Minerals provide surfaces to catalyze reactions
- Cycles of drying and wetting in ponds

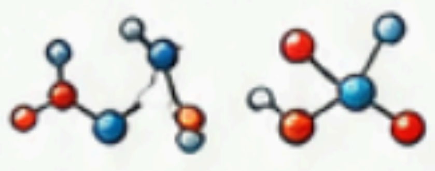
WHY EARTH WAS SPECIAL

- ✓ Right distance from the Sun (habitable zone)
- ✓ Liquid water
- ✓ Suitable atmosphere and pressure
- ✓ Essential elements available
- ✓ Long-term stability

These conditions created the perfect laboratory for chemical evolution.

3 CHEMICAL EVOLUTION: FROM SIMPLE CHEMICALS TO LIFE'S BUILDING BLOCKS

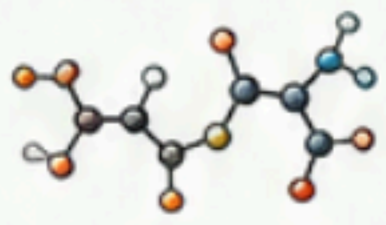
3.1 Simple Inorganic Molecules Form



H_2O CO_2 NH_3 CH_4 H_2 CO

Abundant gases in the early atmosphere and oceans react to form simple molecules.

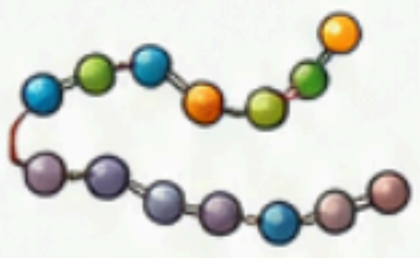
3.2 Formation of Organic Precursors



Energy sources drive reactions that create organic molecules such as:

Amino acids (building blocks of proteins)
Sugars (building blocks of carbohydrates)
Nitrogenous bases (building blocks of DNA/RNA)
Fatty acids (building blocks of lipids)

3.3 Polymerization



Organic monomers link together to form larger polymers:

- Proteins
- Polysaccharides
- Nucleic acids
- Lipids

3.4 Self-Assembly & Protocells

Molecules organize into micelles, vesicles and compartments that can encapsulate molecules and carry out reactions.

3.5 Emergence of Functional Systems

RNA molecules can store information and catalyze reactions (ribozymes). Networks of reactions become more efficient and interconnected.

3.6 Origin of Life (Protocells)

Protocells with membranes, metabolism-like reactions and genetic molecules undergo natural selection and evolve into the first living cells (~3.5–3.8 billion years ago).

IMPORTANT IDEAS

- Life arose from non-living matter by natural laws.
- No single event created life; it was a gradual process.
- Chemical reactions came first, biology later.
- RNA world is a leading hypothesis for early life.

4 THE INTEGRATED STORY: A CONTINUOUS CHAIN OF CAUSES

Big Bang

Creates the universe, space, time and the raw materials (elements).

Stars & Stellar Nucleosynthesis

Make heavier elements like carbon, oxygen, nitrogen—essential for life.

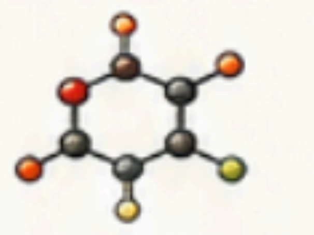
Solar System & Earth Formation

Earth forms from cosmic material and becomes a unique, habitable world.

Early Earth Environments

Water, atmosphere, minerals and energy sources drive rich chemistry.

Chemical Evolution



Simple molecules become complex, self-organizing systems.

Origin of Life

The first living cells emerge and life begins its long evolution.

TIMELINE SNAPSHOT

13.8 bya	Big Bang
4.6 bya	Earth forms
4.4–3.8 bya	Oceans & early atmosphere stabilize
~4.3–3.5 bya	Chemical evolution and protocells
~3.5–3.8 bya	First life appears

(bya = billion years ago)

EVIDENCE THAT SUPPORTS THIS STORY

Cosmic Microwave Background

Leftover radiation from the Big Bang.

Abundance of Light Elements

H, He, Li in the universe matches predictions.

Meteorites & Space Rocks

Contain organic molecules and prebiotic compounds.

Geological Evidence

Oldest rocks (~4.4 bya) show early oceans and Earth's early history.

Laboratory Experiments

Miller–Urey and modern experiments produce organic molecules naturally.

Ancient Microfossils & Isotopes

Stromatolites (~3.5 bya) and carbon isotopes indicate early life.

WHY IT MATTERS

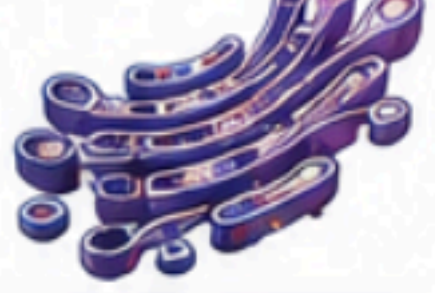
- Explains our connection to the cosmos.
- Helps us understand life's uniqueness and its fragility.
- Guides the search for life on other planets and exoplanets.
- Inspires responsible care for our planet—the only home we know to harbor life.

WE ARE STAR-STUFF, EARTH IS OUR HOME, AND LIFE IS NATURE'S MOST EXTRAORDINARY OUTCOME.
UNDERSTANDING OUR ORIGIN HELPS US VALUE AND PROTECT LIFE.

5.(a) ORIGIN AND EVOLUTION OF THE ENDOPLASMIC RETICULUM (ER)

Two Models for the Origin of ER and Its Evolutionary Link to Protein Secretion and Golgi Apparatus

The endoplasmic reticulum (ER) is a defining feature of eukaryotic cells, forming an extensive membrane network involved in protein and lipid synthesis, folding and intracellular transport.

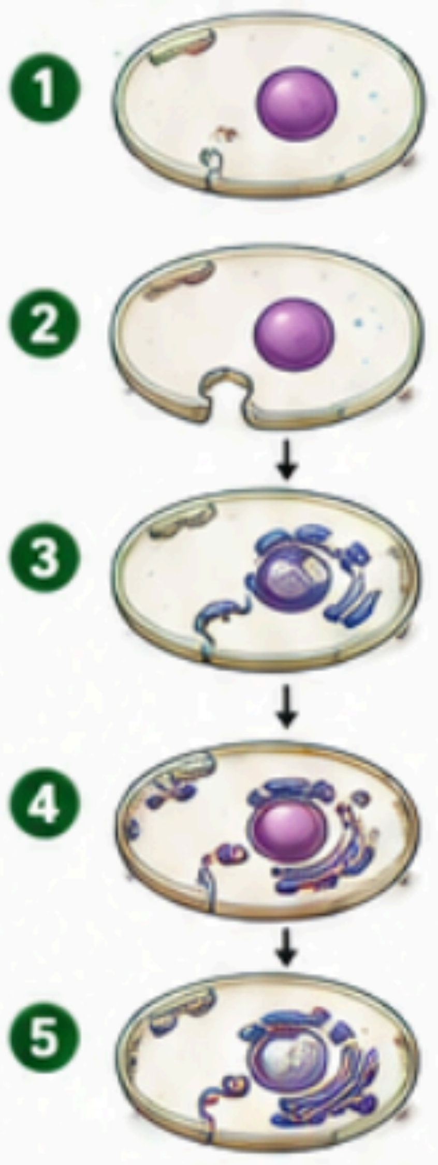


TWO MODELS PROPOSED FOR THE ORIGIN OF ER IN EUKARYOTES

1. THE "AUTOGENOUS" (INTERNAL ORIGIN) MODEL
(Whittaker, 1969)

ER evolved from infoldings of the plasma membrane of the ancestral eukaryotic cell.

Proposed steps:



1. Ancestral eukaryote with plasma membrane containing enzymes for lipid synthesis.
2. Invagination (infolding) of the plasma membrane increases surface area.
3. Infoldings pinch off to form an internal membrane network that remains continuous with the outer membrane.
4. Membranes differentiate: some regions become rough ER (rER) with ribosomes for protein synthesis.
5. Further specialization leads to smooth ER (sER) (lipid synthesis, detoxification, Ca2+ storage).

TWHAT IS ER?

A dynamic network of membranes including:

- **Rough ER (rER):** studded with ribosomes; site of protein synthesis and initial processing.
- **Smooth ER (sER):** site of lipid synthesis, detoxification and Ca2+ storage.

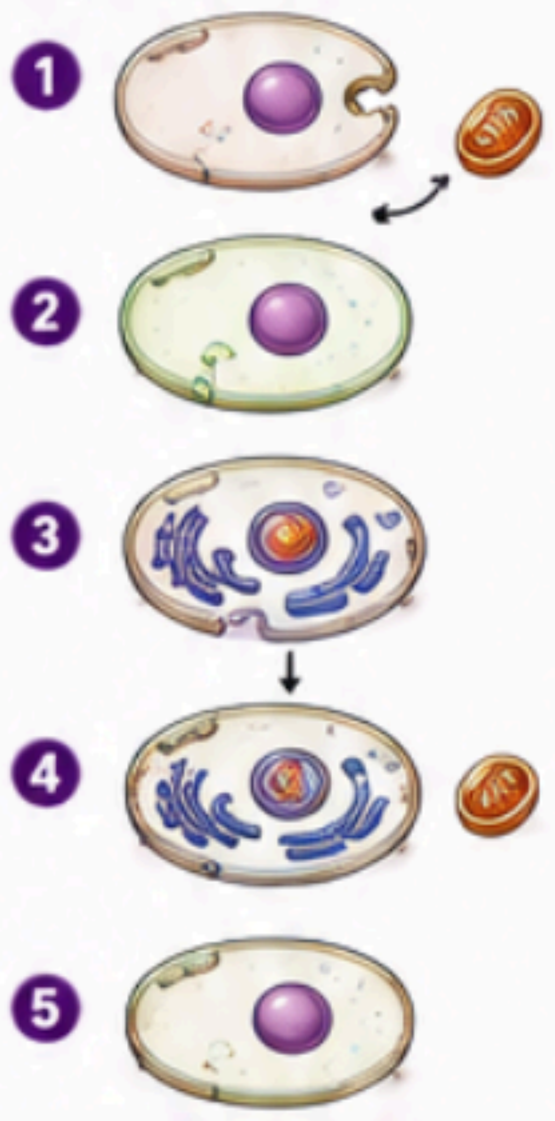
Functions:

- Protein synthesis and folding (rER)
- Lipid synthesis (sER)
- Transport of molecules
- Calcium homeostasis
- Detoxification
- Membrane biogenesis

2. THE "ENDOSYMBIOTIC" MODEL
(de Duve, 1991)

ER evolved from the internal membranes of an engulfed aerobic bacterium (alpha-proteobacterium ancestor of mitochondria).

Proposed steps:



1. Ancestral host cell (archaeon-like). Engulfs an aerobic bacterium.
2. Bacterium survives inside host as an endosymbiont.
3. Extensive membrane systems of the endosymbiont spread throughout host cytoplasm.
4. These membranes give rise to ER network; endosymbiont becomes mitochondrion.
5. ER evolves as a widespread membrane system in the eukaryotic cell.

Supporting Evidence

- Continuity of ER membrane with nuclear envelope and plasma membrane.
- Similar lipid composition of plasma membrane and ER.
- Presence of ER in cells lacking mitochondria (e.g., some protists) suggests ER evolved independently.

Key

▭	Plasma membrane
●	Nucleus
•	Ribosome
⊂⊃	ER membrane

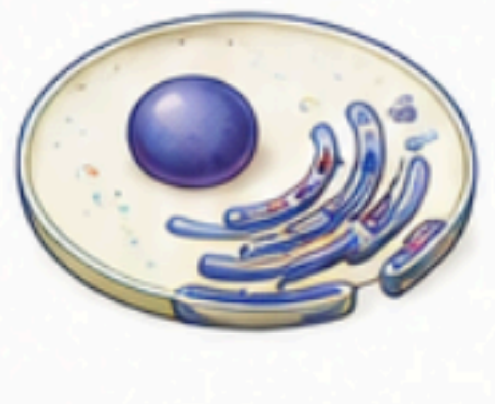
Supporting Evidence

- Similarity between ER and bacterial membranes (lipid composition, proteins involved in translation).
- Ribosomes on rER are similar to bacterial ribosomes.
- ER membrane proteins (e.g., Sec61 translocon) are homologous to bacterial protein translocation systems.

HOW ER EVOLUTION IS LINKED TO PROTEIN SECRETION PATHWAYS AND GOLGI APPARATUS

1. Ancestral State: Early Eukaryote

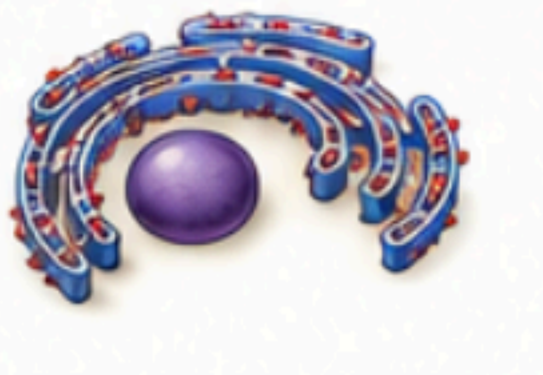
Basic cell with plasma membrane and internal membrane infoldings (early ER).



- Proteins mostly function inside the cell, little or no secretion.

2. Emergence of Rough ER

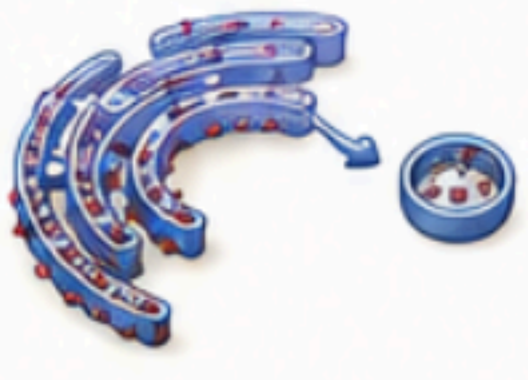
Ribosomes bind to ER membranes. Proteins are synthesized into the ER lumen or membrane.



- Co-translational translocation of proteins into rER.
- Signal peptides and translocon systems evolve.

3. Vesicle Formation and Transport

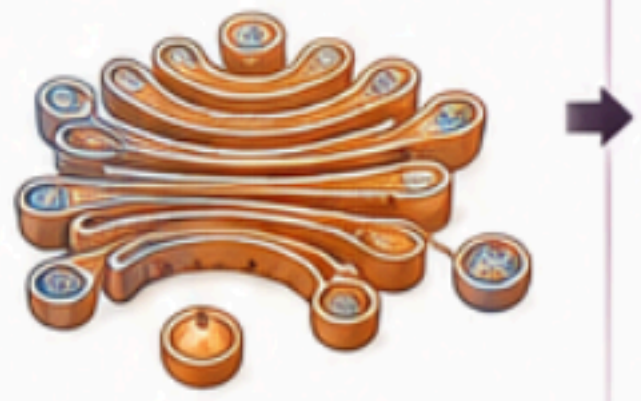
Budding of transport vesicles from ER enables movement of proteins to other compartments.



- COPII-coated vesicles evolve (anterograde transport).
- SNARE proteins and Rab GTPases mediate targeting and fusion.

4. Origin of Golgi Apparatus

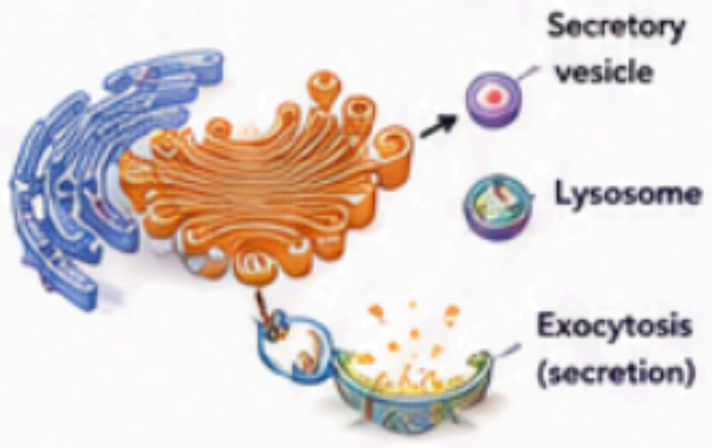
Stacked cisternae (Golgi) arise from modification and specialization of vesicle-targeting membranes.



- Early Golgi-like compartments enable further modification and sorting.
- Enzymes for glycosylation and sulfation evolve.

5. Advanced Secretory Pathway in Modern Eukaryotes

Integrated ER–Golgi–vesicle system orders proteins to plasma membrane, lysosomes or extracellular space.



- Constitutive and regulated secretion.
- Complex sorting signals.
- Enables multicellularity, extracellular matrix, hormones, enzymes, etc.

Key Evolutioary Innovations

✓ Increase in membrane surface area (ER) allowed large-scale protein synthesis.
✓ Compartmentalization improved efficiency and quality control.
✓ Vesicular trafficking and Golgi enabled directed transport and secretion.
✓ Secretion pathways were crucial for cell communication, defense, and multicellularity.

Evidence for ER–Golgi Co-evolution

- Structural continuity in early eukaryotes (e.g., yeast, protists).
- Functional interdependence: ER exports, Golgi modifies and sorts.
- Conserved machinery (SNAREs, coat proteins, GTPases) throughout eukaryotes.

COMPARISON OF THE TWO MODELS

Feature	Autogenous Model	Endosymbiotic Model
Source	Plasma membrane infoldings	Endosymbiont (proto-mitochondrion membranes)
Continuity	Continuous with plasma membrane	Derived from internal bacterial membranes
Key Proponent	Whittaker (1969)	de Duve (1991)
Main Support	Membrane continuity, lipid similarity	Protein machinery similarity, bacterial-like features
Limitations	Does not explain bacterial-like features of ER	Does not explain continuity with plasma membrane

Most Accepted View

A combination or synthesis of both models: ER may have evolved from plasma membrane infoldings with contribution from endosymbiotic membranes.

BIOLOGICAL SIGNIFICANCE

Efficient Protein Production:
rER enables high-yield synthesis and folding.

Directed Secretion:
Proteins are delivered to the right destination.

Cell Communication & Interaction:
Secretion allows signaling molecules, enzymes and receptors.

Multicellularity & Complexity:
Secretion and extracellular components are essential for tissue formation and organismal complexity.

Evolutionary Success:
The ER–Golgi system is a hallmark of eukaryotic cells and underlies their diversity and adaptability.

KEY TAKE-HOME MESSAGES

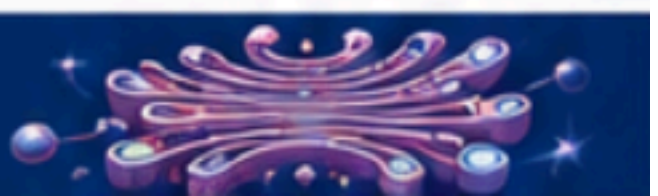
☑ Two main models explain ER origin: autogenous (from plasma membrane infoldings) and endosymbiotic (from engulfed bacterium).

☑ ER evolution enabled compartmentalization and large-scale protein synthesis.

☑ Vesicular transport and Golgi apparatus evolved to modify, sort and direct proteins.

☑ The ER–Golgi–secretory pathway was a major driver in the evolution of complex eukaryotic cells and multicellular life.

From simple membranes to a sophisticated trafficking network— the ER and Golgi apparatus power eukaryotic life.



8. (b) Catastrophic, Mass, and Background Extinctions: Differences and Examples from Earth's History

Extinction is the natural or caused disappearance of species from Earth. Extinctions occur at different scales. They can be grouped into three types.

Feature	Catastrophic Extinction	Mass Extinction	Background Extinction
Definition	A short-term, sudden event caused by a catastrophic phenomenon that leads to the rapid loss of many species.	A relatively short geological interval in which a very large proportion of species on Earth go extinct across wide regions.	The normal, ongoing extinction that occurs steadily over long periods due to natural causes.
Scale & Rate	Sudden (days to thousands of years); affects many species but generally not all life.	Rapid on geological time scale (thousands to millions of years); affects a large percentage of species globally.	Very slow and continuous; affects a few species at a time.
Extent of Species Loss	Moderate to high, but limited in duration and often regionally variable.	Very high; typically >75% of species on Earth.	Low; usually <1–5 species per million species per year.
Duration	Short (instantaneous to tens of thousands of years).	Relatively short in geological terms (hundreds of thousands to a few million years).	Continuous over millions of years.
Causes	Sudden catastrophic events like impact, volcanic eruption, mega-tsunami, asteroid airbursts, etc.	Major global disturbances such as large-scale volcanism, asteroid impacts, climate change, ocean anoxia, sea-level change.	Natural ecological competition, environmental changes, disease, predation, random events.
Examples	• Chicxulub impact (66 Ma) – rapid loss of many species including non-avian dinosaurs • Krakatoa eruption (1883 CE) – devastated local ecosystems	• End-Permian (252 Ma) • End-Triassic (201 Ma) • End-Cretaceous (66 Ma) • Late Devonian (375 Ma) • Ordovician–Silurian (444 Ma)	Ordinary extinctions observed throughout Earth's history (e.g., extinction of many insect species, small mammals, plants, etc.).
Impact on Evolution	Can cause abrupt ecological collapse and open niches for new species.	Reshapes life on Earth; leads to radiation of new groups and major evolutionary transitions.	Maintains ecological balance; drives gradual evolution and species turnover.
Recovery Time	Relatively quick (thousands to hundreds of thousands of years).	Long (millions of years for full recovery of ecosystems).	Ongoing; no "recovery" needed as it is a continuous process.

TIMELINE OF MAJOR MASS EXTINCTIONS

Ordovician–Silurian Extinction
~444 million years ago
Occurs during glaciation and sea-level fall.
~86% of marine species lost.

Late Devonian Extinction
~375 million years ago
Likely caused by climate cooling, sea-level change and ocean anoxia.
~75% of species lost.

End-Permian ("Great Dying")
~252 million years ago
Caused by massive volcanism, climate change, ocean anoxia.
~96% of marine species and 70% of terrestrial species lost.

End-Triassic Extinction
~201 million years ago
Associated with volcanic activity, CO_2 increase, ocean acidification.
~80% of species lost.

End-Cretaceous Extinction
~66 million years ago
Triggered by asteroid impact and Deccan volcanism.
Non-avian dinosaurs and many species lost.

444 Ma → 375 Ma → 252 Ma → 201 Ma → 66 Ma

KEY POINTS

- ☑ All three types of extinction are natural and have shaped the evolution of life.
- ☑ Mass extinctions are rare but dramatic events.
- ☑ Catastrophic extinctions are sudden and often caused by short-lived events.
- ☑ Background extinctions are continuous and form the baseline of biodiversity loss.

EXAMPLES AT A GLANCE

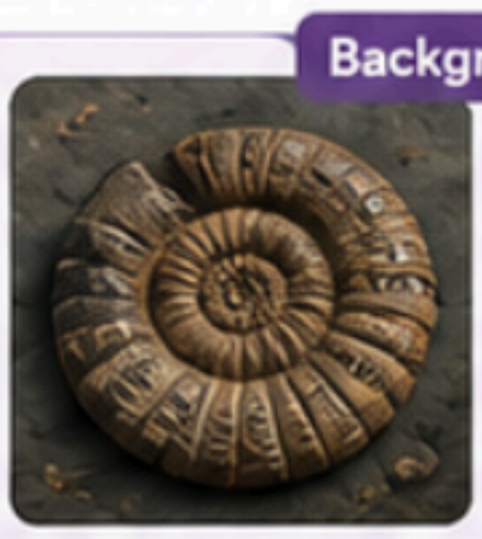
Catastrophic Extinction

- Chicxulub impact (66 Ma) – caused global darkness, cooling and collapse of food chains.
- Krakatoa eruption (1883 CE) – caused tsunamis, climate effects and regional extinctions.

Mass Extinction

- End-Permian – "Great Dying" was the most severe.
- End-Cretaceous – led to the extinction of dinosaurs and rise of mammals.

Background Extinction



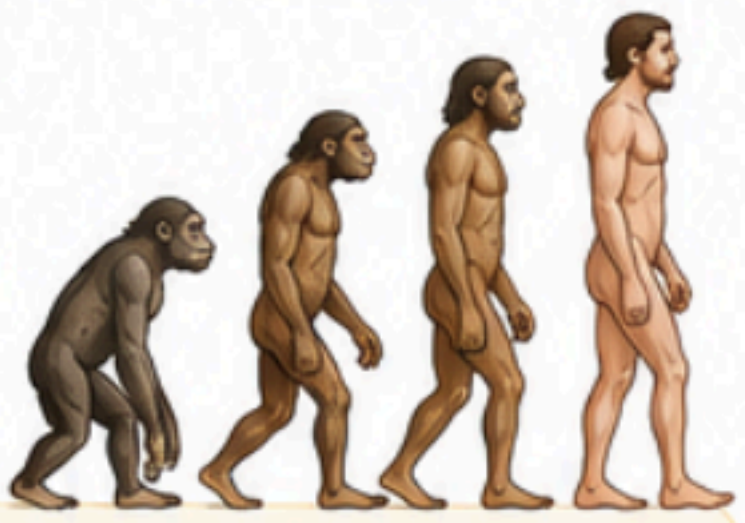
- Ongoing loss of species like certain insects, amphibians, and plants.
- Natural species turnover over geological time.

In Summary: Catastrophic extinctions are sudden and event-driven; mass extinctions are large-scale and geologically brief; background extinctions are slow and continuous. Together, they have been powerful forces shaping life on Earth.

9.

What Makes Modern Humans Unique?

Anatomical and Genetic Traits that Distinguish Homo sapiens from Other Hominins and Great Apes

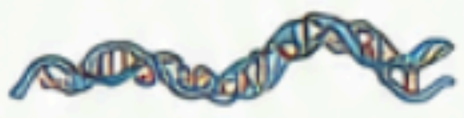


Modern humans (*Homo sapiens*) share a recent common ancestor with other hominins and great apes, yet we possess a distinctive combination of anatomical features and genetic innovations that underpin our **cognitive, behavioral and cultural uniqueness.**

A. ANATOMICAL TRAITS

Feature	How Modern Humans Are Unique
Larger, more complex brain	• Average brain size ~1,350 cm³ (vs. ~400–550 cm³ in great apes). • Expanded neocortex, especially in prefrontal, parietal and temporal regions—supporting abstract thought, planning, language and self-awareness.
High, rounded cranium & vertical forehead	• Tall, globular cranium with diminished brow ridges. • Greater cranial vault capacity for higher cognitive functions.
Reduced face and jaws	• Flatter face, smaller jaws and teeth. • Chin (mental eminence) present—unique to modern humans, related to speech and facial musculature.
Fine motor sophistication of the hand	• Longer thumb relative to fingers; precision grip. • Enhanced dexterity for tool making, art and complex manipulation. • Unique hand proportions for power and precision.
Bipedalism fully optimized	• S-shaped spine for balance and shock absorption. • Bowl-shaped pelvis, valgus knee, arched foot—maximize efficient, endurance walking/running.
Reduced body hair & increased thermoregulation	• Less body hair, more eccrine sweat glands—better heat dissipation. • Allowed endurance activity in hot climates.
Voice and speech anatomy	• Lowered larynx, descended hyoid bone, and restructured vocal tract. • Enables wide range of speech sounds and complex language.
Sensory & visual refinements	• High visual acuity and color perception. • Fovea centralis densely packed for detailed vision. • Enhanced integration of sensory information in the brain.

B. GENETIC TRAITS

Genetic Feature	How It Distinguishes Modern Humans
FOXP2 gene (modified form)	• Human-specific changes enhance neural circuits for speech and language. • More efficient production and sequencing of vocalizations.
HAR1 (Human Accelerated Region 1) 	• DNA sequence highly accelerated in humans. • Involved in cortical development and regulation of genes for brain growth.
SRGAP2C gene (human-specific duplication)	• Originated ~2–3 million years ago. • Promotes neocortical expansion and connectivity—linked to advanced cognition.
Microcephalin (MCPH1) variant	• Human-specific variant associated with increased brain size by regulating neural progenitor cells.
Olfactory receptor gene loss	• Fewer functional olfactory receptor genes (~25% pseudogenes). • Less reliance on smell; shift toward vision, hearing and higher cognition.
Immune system gene adaptations	• Unique alleles (e.g., HLA diversity, TLR variations) show adaptation to diverse pathogens and environments.
Lactase persistence alleles (in many populations)	• Ability to digest lactose into adulthood—a cultural and nutritional advantage that spread with dairying.
Metabolic & energy regulation	• Genetic variants improve efficiency, endurance and brain energy metabolism (e.g., PPARA, AMY1 copy number variation).

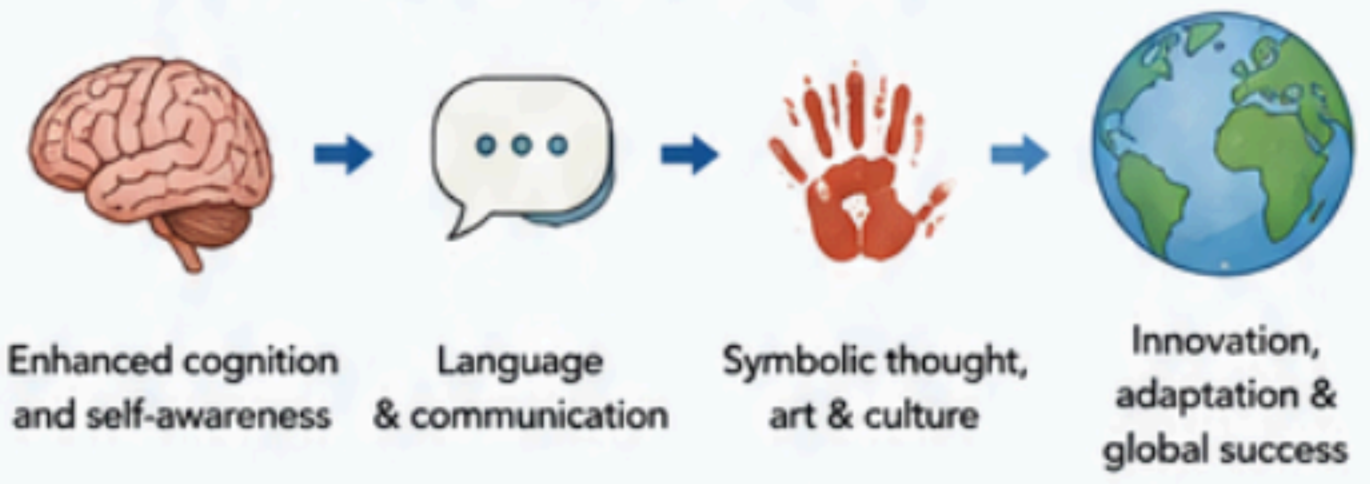
C. COMPARATIVE SNAPSHOT

Trait Category	Great Apes (e.g., Chimpanzee)	Other Hominins (e.g., Neanderthals)	Modern Humans (*Homo sapiens*)
Brain size	~400–500 cm³	~1,200–1,750 cm³	~1,300–1,450 cm³ (optimized organization)
Forehead & Brow	Low forehead, prominent brow ridges	Lower forehead, some brow ridges	High, vertical forehead; minimal brow ridges
Face & Jaw	Prognathous; large jaws & canines	Mid-facial projection; no chin	Flat face; small jaws; distinct chin
Chin	Absent	Absent	Present (mental eminence)
Language Ability	Limited vocalizations	Likely spoken language rudimentary	Complex, symbolic, recursive language
Tools & Culture	Simple tools; learned behaviors	Advanced tools; culture present	Highly complex tools, art, symbolism, technology, writing
Genetics	Ancestral state	Shared many genes with us	Unique genetic changes shaping brain, speech, immunity, metabolism, etc.

KEY TAKEAWAYS

- ☑ Modern humans combine unique anatomical adaptations (brain, face, hands, posture, speech) with distinctive genetic innovations.
- ☑ These changes enabled advanced cognition, language, culture, technology, and global dispersal.
- ☑ We are not just bigger-brained apes—our biology and genes reflect a unique evolutionary path.

EVOLUTIONARY SIGNIFICANCE



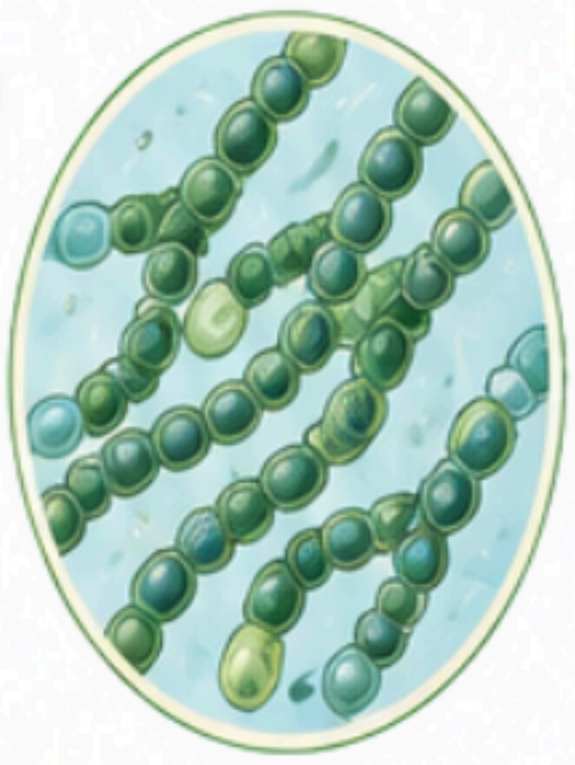
Enhanced cognition and self-awareness → Language & communication → Symbolic thought, art & culture → Innovation, adaptation & global success

IN SUMMARY

Modern humans (*Homo sapiens*) are distinguished by a unique suite of anatomical features and genetic modifications that together underlie our exceptional cognitive abilities, cultural complexity and capacity to shape our world.

8. (a)

The Role of Cyanobacteria in Transforming Earth's Early Environment and Enabling the Evolution of Complex Life

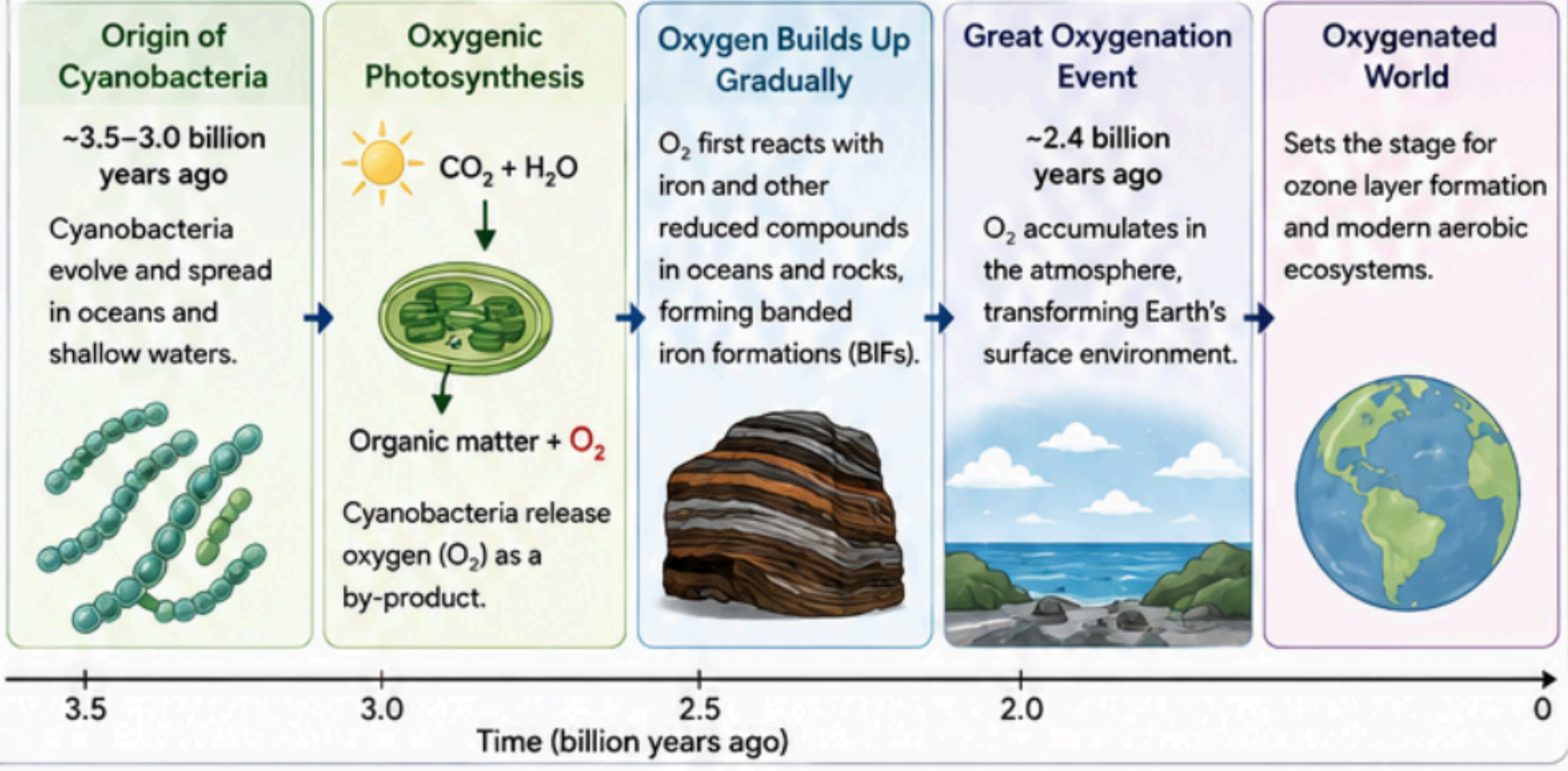


Cyanobacteria (blue-green algae) are ancient photosynthetic prokaryotes that profoundly changed Earth's environment through oxygenic photosynthesis, paving the way for complex life.

1. EARTH BEFORE CYANOBACTERIA

- **~4.6 billion years ago:** Earth had a reducing atmosphere with little or no free oxygen.
- Life was limited to simple anaerobic microbes.
- High volcanic activity, intense UV radiation, and frequent impacts characterized the early Earth.

2. THE GREAT OXYGENATION: CYANOBACTERIAL IMPACT



Origin of Cyanobacteria

~3.5–3.0 billion years ago

Cyanobacteria evolve and spread in oceans and shallow waters.

Oxygenic Photosynthesis

$CO_2 + H_2O$ → Organic matter + O_2

Cyanobacteria release oxygen (O_2) as a by-product.

Oxygen Builds Up Gradually

O_2 first reacts with iron and other reduced compounds in oceans and rocks, forming banded iron formations (BIFs).

Great Oxygenation Event

~2.4 billion years ago

O_2 accumulates in the atmosphere, transforming Earth's surface environment.

Oxygenated World

Sets the stage for ozone layer formation and modern aerobic ecosystems.

3. HOW CYANOBACTERIA TRANSFORMED EARTH'S ENVIRONMENT

Released Oxygen

Oxygenic photosynthesis released O_2, changing a reducing atmosphere to an oxidizing one.

Ozone Layer Formation

O_2 in the upper atmosphere formed ozone (O_3), which absorbed harmful UV radiation, protecting life on land.

Changed Ocean Chemistry

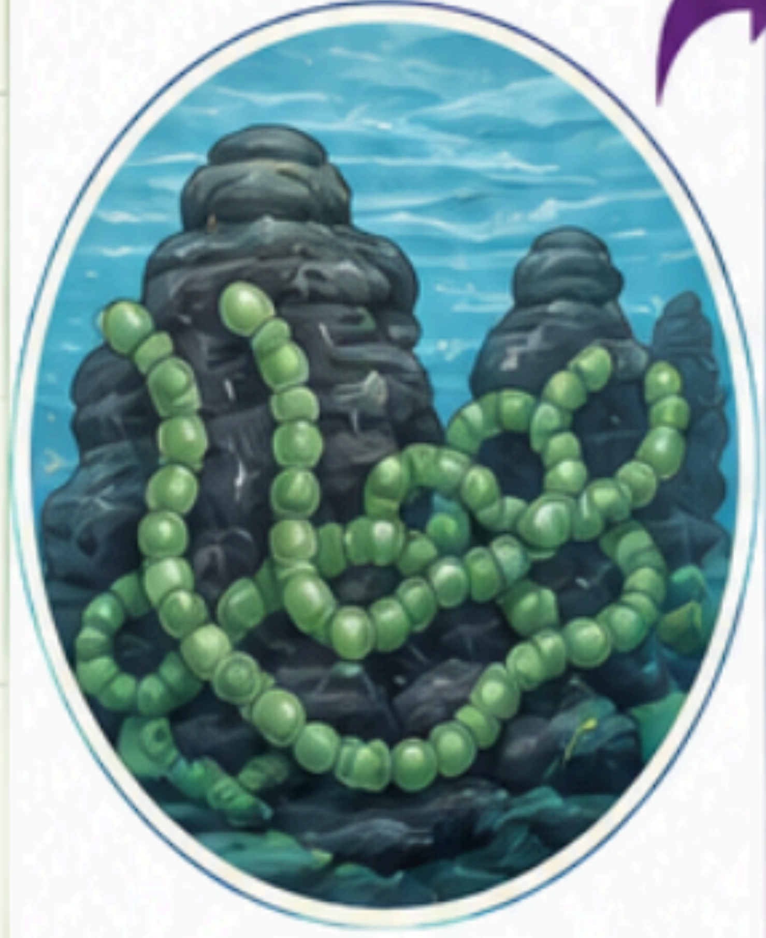
Altered pH and redox conditions, enabling new biogeochemical cycles (carbon, nitrogen, sulfur).

Created New Habitats

Shallow, oxygenated waters and surfaces supported diverse microbial communities and stromatolite formation.

Facilitated Nutrient Cycling

Promoted stable ecosystems through enhanced organic matter production and mineral cycling.



Stromatolites built by cyanobacteria (~3.5 billion years ago)

4. HOW THIS CHANGE ENABLED THE EVOLUTION OF COMPLEX LIFE

Energy for Complex Cells

Oxygen allowed the evolution of aerobic respiration, which is far more energy-efficient than anaerobic metabolism.

Endosymbiosis

Aerobic bacteria (alpha-proteobacteria) were engulfed by host cells, evolving into mitochondria—powerhouses of eukaryotic cells (~1.5–2.0 Ga).

Rise of Eukaryotes

Eukaryotic cells with nucleus and organelles evolved, leading to greater size, complexity, and specialization.

Multicellularity and Diversification

Enabled the evolution of multicellular algae, animals, and plants, and ultimately the diverse life we see today.

Life on Land

The ozone layer and oxygen-rich environment allowed colonization of land and the radiation of complex organisms.

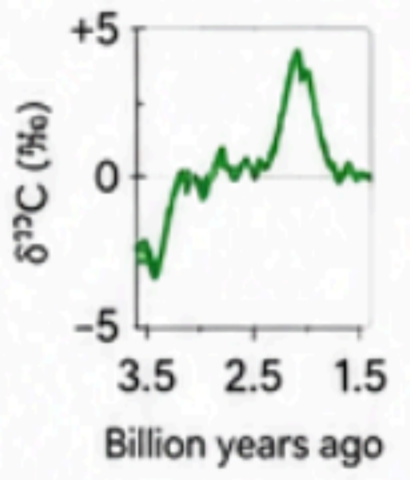
5. EVIDENCE FOR CYANOBACTERIAL IMPACT

Banded Iron Formations (BIFs)

Layered rocks formed by oxygen reacting with iron in ancient oceans (~3.8–1.8 Ga).

Stromatolites

Fossilized structures built by cyanobacteria in shallow waters (~3.5 Ga to recent).



Carbon Isotope Signatures

Shifts in $\delta^{13}C$ indicate extensive photosynthesis by ancient cyanobacteria.

Microfossils

Fossilized cyanobacterial cells preserved in ancient rocks (~3.2–2.0 Ga).

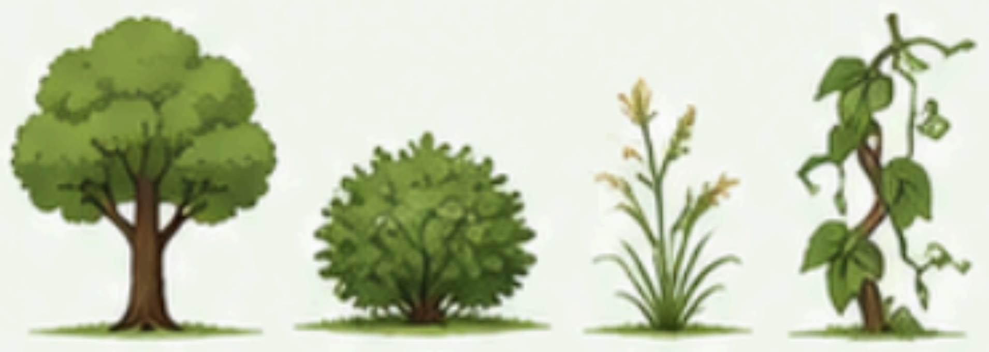
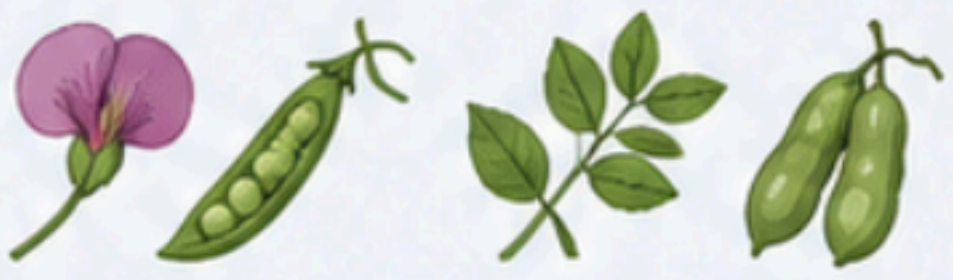
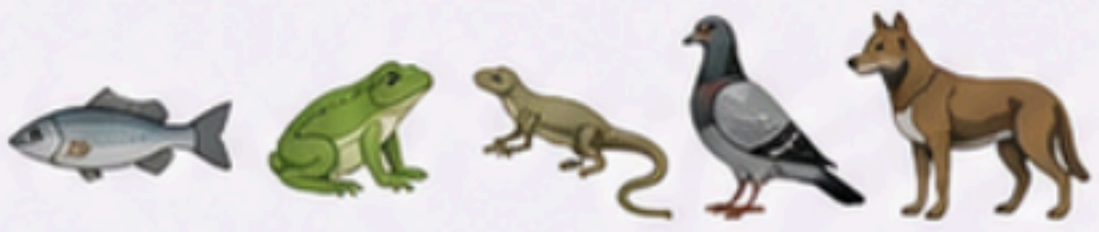
IN SUMMARY

Cyanobacteria were the architects of Earth's transformation. By releasing oxygen, they changed the planet's atmosphere, protected life with the ozone layer, and created the conditions necessary for the evolution of complex cells, multicellular organisms, and the rich biodiversity we see today.

7.(a)

Differences Between Artificial, Natural, and Phylogenetic Systems of Classification

Systems of classification arrange organisms into groups. They differ in the basis used, the naturalness of groups formed, and how well they reflect evolutionary relationships.

Feature	Artificial System	Natural System	Phylogenetic System
Basis of classification	• Based on one or a few easily observable characters only, without considering relationships.	• Based on many characters (morphological, anatomical, physiological, etc.), but not necessarily evolutionary relationships.	• Based on evolutionary relationships and common ancestry (descent with modification).
Nature of groups formed	• Groups are unnatural or arbitrary; may place unrelated organisms together and separate related ones.	• Groups are more natural and reflect overall similarity. Most related organisms are kept together.	• Groups are natural and monophyletic (include a common ancestor and all its descendants).
Main focus	• Convenience and simplicity.	• Overall similarity and natural affinity.	• Evolutionary history and phylogeny.
Examples of classification (Scientists)	• Carolus Linnaeus (early system) used few characters like habit, habitat, number of stamens, etc. **Example:** Plantae divided into trees, shrubs, herbs, climbers. 	• A. L. de Jussieu, Bentham & Hooker **Example:** Plants grouped by many characters – e.g., Fabaceae (pea, gram, bean, etc.) based on flower, fruit, leaf, etc. 	• Haeckel, Copeland, Dobzhansky, (and modern phylogenetic systems using molecular data) **Example:** Animals grouped according to evolutionary relationships – Vertebrata divided into fishes, amphibians, reptiles, birds, mammals. 
Key limitation	• Ignores many important characters and evolution; not reliable for showing relationships.	• Does not show the direction of evolution or ancestral descent.	• Requires more data and analysis; can be complex but most informative.

Importance in Studying Relationships and Evolution

Artificial System

- Helpful as a starting point for arranging and identifying organisms.
- Useful for beginners and for practical purposes (e.g., herbal groups, agriculture).

Relationship & Evolution:
Limited help; does not reveal true relationships or evolutionary history.

Natural System

- Shows natural relationships based on many characters.
- Helps in predicting characters of organisms and understanding similarities and differences.

Relationship & Evolution:
Better reflection of relationships; indirect help in understanding evolution but does not show ancestry.

Phylogenetic System

- Reveals evolutionary relationships and ancestry.
- Helps reconstruct evolutionary pathways and explains diversity of life.

Relationship & Evolution:
Most significant; best for understanding evolution, common ancestry, and diversification of organisms.

In summary: Artificial systems are convenient but unnatural; Natural systems are more natural and informative; Phylogenetic systems are evolutionary and provide the truest picture of relationships and the origin of life.

7 (b) Taxonomy: Components and Types

Taxonomy is the science of identification, naming, classification and description of organisms.

A. COMPONENTS OF TAXONOMY

Taxonomy involves several interrelated components that together help in the study and organization of biodiversity.

1 Identification

Recognition of an organism and determining its identity using observations, keys, and literature.

Example:
Identifying a mango tree as *Mangifera indica*.

2 Nomenclature

Mangifera indica L.

Assigning scientific names to organisms according to established rules (International Code of Nomenclature).

Example:
Mangifera indica L. (L. = Linnaeus, the author).

3 Classification

Arranging organisms into groups or categories based on similarities and relationships.

Example:
Mango → Plantae → Angiosperms → Rosales → Anacardiaceae → *Mangifera* → *M. indica*

4 Description

Detailed account of morphology, structure, anatomy, habitat and other features of an organism.

Example:
Description of *Rana tigrina*: body measurements, skin texture, habitat, etc.

5 Typification

Designation and preservation of type specimens (holotype, lectotype, etc.) to provide a reference for a name.

Example:
A pressed specimen of *Rosa indica* designated as holotype.

6 Documentation & Information Management

Recording, storing and sharing taxonomic data through herbaria, museums, databases and publications.

Example:
Data in Kew *Plants of the World Online* (POWO).

B. TYPES OF TAXONOMY

Taxonomy has evolved from traditional methods to modern and molecular approaches to understand diversity and evolutionary relationships.

	1. Classical (Traditional) Taxonomy	2. Modern (Integrative) Taxonomy	3. Molecular Taxonomy (Contemporary Approach)
Basis	Morphology, anatomy, cytology, embryology, palynology, and comparative studies.	Uses all available data – morphological, anatomical, embryological, ecological, biochemical, cytological, behavioral, and paleontological.	Uses DNA/RNA sequences, proteins and other molecular markers to study relationships.
Approach	Descriptive; based mainly on observable characters.	Integrative; combines multiple lines of evidence.	Analytical; based on genetic and molecular data.
Tools Used	Simple microscope, hand lens, keys, herbarium specimens, comparative morphology.	Microscope, SEM, chromatographs, biochemical tests, ecological studies, statistical methods.	PCR, DNA sequencing, gel electrophoresis, bioinformatics, phylogenetic software.
Nature of Classification	Largely artificial or natural; based on limited characters.	More natural; reflects overall similarity and evolutionary relationships.	Evolutionary (phylogenetic); reflects genetic relationships and common ancestry.
Example	Bentham & Hooker's classification of flowering plants (based on morphology).	APG system of Angiosperm classification (uses morphology + molecular + other data).	Classification of organisms using rRNA gene sequences; Human beings placed in Primates based on DNA evidence.
Outcome	Useful for identification and naming; limited understanding of relationships.	More accurate classification; better understanding of diversity and evolution.	Highly accurate; reveals hidden relationships, cryptic species and evolutionary history.

EXAMPLES AT A GLANCE

Classical Taxonomy
- Identifying *Hibiscus rosa-sinensis* using flower characters.
- Classifying animals using skeletal features (e.g., birds vs. mammals).

Modern Taxonomy
- Classification of *Rana tigrina* using morphology, karyotype, calls and ecological data.
- APG IV classification of angiosperms.

Molecular Taxonomy
- Using DNA barcoding (COI gene) to identify species of insects.
- Phylogenetic tree of living beings constructed from rRNA gene sequences.

KEY TAKEAWAY

Taxonomy provides the framework to discover, organize and understand the diversity of life. From classical observations to modern integrative methods and molecular data, taxonomy continues to reveal the evolutionary relationships among organisms.

ROLE OF HORIZONTAL GENE TRANSFER (HGT) IN EVOLUTION

Genes can move across species boundaries – driving evolution beyond inheritance.

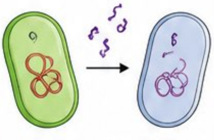
1. WHAT IS HORIZONTAL GENE TRANSFER (HGT)?

Horizontal gene transfer is the movement of genetic material between organisms other than by vertical transmission (parent to offspring).

- ▶ Occurs between unrelated individuals, even across species and kingdoms.
- ▶ Major in prokaryotes, also occurs in eukaryotes.

2. MAJOR MECHANISMS OF HORIZONTAL GENE TRANSFER

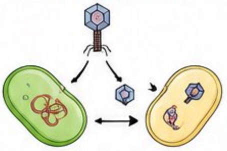
(i) TRANSFORMATION



Uptake of naked DNA from the environment by a competent cell.

Example: Uptake of free DNA from dead bacteria by *Streptococcus pneumoniae*.

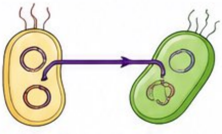
(ii) TRANSDUCTION



Transfer of DNA from one bacterium to another by a bacteriophage.

Example: Phage P1 transferring genes between *E. coli* cells.

(iii) CONJUGATION



Direct transfer of DNA (usually plasmid) through cell-to-cell contact via a pilus.

Example: Transfer of F plasmid between *E. coli* cells.

3. SOURCES OF HGT

- Plasmids
- Transposons
- Integrons
- Bacteriophages
- Genomic islands
- Pathogenicity islands

Plasmid

5. WHERE DOES HGT OCCUR?

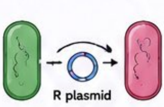
- Common in bacteria and archaea.
- Occurs in eukaryotes too, though less frequent.
- Examples: mitochondria, chloroplasts (endosymbiotic gene transfer); fungi, plants, animals.
- Important in microbial communities (biofilms, gut microbiota, soil).

4. IMPORTANCE OF HGT IN EVOLUTION

1. Rapid Acquisition of New Traits	Provides immediate adaptive advantage without waiting for slow mutations.
2. Antibiotic Resistance	Spread of resistance genes among bacteria (e.g., β-lactamase genes).
3. Virulence and Pathogenicity	Transfer of toxin or virulence genes increases survival in host organisms.
4. Metabolic Innovation	Introduction of new metabolic pathways, enabling use of novel substrates.
5. Symbiosis and Adaptation	Facilitates adaptation to new environments and establishment of symbiosis.
6. Shaping Genome Evolution	Creates genetic mosaicism, increases genomic diversity and complexity.

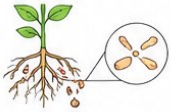
6. EXAMPLES OF HGT AND EVOLUTIONARY IMPACT

Antibiotic Resistance



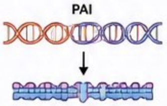
Plasmid carrying resistance gene spreads via conjugation, leading to multi-drug resistant strains.

Nitrogen Fixation



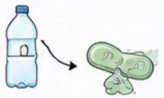
nitrogenase genes transferred between bacteria, enabling nitrogen fixation in new bacterial hosts.

Pathogenicity Islands



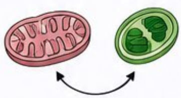
Pathogenicity islands acquired by HGT encode toxins, secretion systems and virulence factors.

Degradation Pathways



Genes for degradation of novel compounds (e.g., plastics, hydrocarbons) spread by HGT.

Eukaryotic Adaptations



Genes transferred from endosymbionts to host nucleus help in organelle function and adaptation.

7. EVOLUTIONARY SIGNIFICANCE

- ✓ Accelerates evolution beyond vertical inheritance.
- ✓ Introduces novel genes into populations.
- ✓ Allows organisms to colonize new niches.
- ✓ Creates genetic diversity and mosaic genomes.
- ✓ Important in early evolution of life.
- ✓ Blurs species boundaries and gene flow.

8. LIMITATIONS OF HGT

- ☒ Not all transferred genes are useful.
- ☒ Requires compatibility of DNA and cellular machinery.
- ☒ May be lost if not beneficial.
- ☒ Less stable in multicellular eukaryotes.

9. KEY POINTS TO REMEMBER

- ★ HGT moves genes across species.
- ★ Three main mechanisms: transformation, transduction and conjugation.
- ★ Drives adaptation, diversity and evolution.
- ★ Crucial in antibiotic resistance and emergence of pathogens.
- ★ Important in both prokaryotes and eukaryotes.

10. FREQUENTLY ASKED EXAM QUESTIONS

1. What is horizontal gene transfer?
2. Describe the mechanisms of HGT.
3. Discuss the role of HGT in evolution.
4. Give examples of HGT and their significance.
5. How does HGT differ from vertical gene transfer?

11. MEMORY TRICK

"TTC – Transfer That Changes"

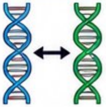
T – Transformation
T – Transduction
C – Conjugation

12. IN SHORT

Horizontal gene transfer is a powerful evolutionary force that enables rapid acquisition of beneficial genes, enhances adaptability, and shapes the genetic diversity of organisms.

MOLECULAR DRIVE vs MOLECULAR DIVERGENCE

MOLECULAR DIFFERENCES

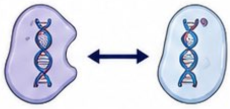


Molecular drive leads to similarity, whereas molecular divergence leads to difference.

1. MOLECULAR DRIVE

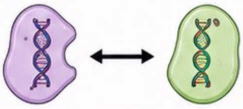
- Process by which related organisms become more similar at the molecular level.
- It reduces differences.
- Acts towards uniformity.
- Results from stabilizing or purifying selection.

Molecular Drive (Similarity)



More similarity at DNA, RNA and protein level

Molecular Divergence (Difference)



More differences at DNA, RNA and protein level

2. MOLECULAR DIVERGENCE

- Process by which related organisms become more different at the molecular level.
- It increases differences.
- Acts towards variability.
- Results from accumulating changes (natural selection, mutation, drift, adaptive radiation, etc.).

3. MOLECULAR DIFFERENCES BETWEEN DRIVE AND DIVERGENCE

Feature	Molecular Drive	Molecular Divergence
1. Direction of Change	Towards similarity; reduces differences.	Towards difference; increases differences.
2. Genetic Changes	Conservative changes; elimination of variation.	Accumulative changes; increase in variation.
3. Type of Selection	Stabilizing (purifying) selection.	Diversifying selection, disruptive selection, neutral drift, adaptive selection.
4. Molecular Level Affected	DNA sequences, RNA and proteins become more conserved.	DNA sequences, RNA and proteins become more variable.
5. Evolutionary Outcome	Evolutionary conservatism; preservation of essential functions.	Evolutionary change; leads to new functions and adaptations.
6. Examples	Conserved genes (e.g., histones, rRNA, actin), housekeeping genes.	Immune genes, globin genes, reproductive proteins, new enzymes.
7. Substitution Rate	Low rate of substitution; high conservation.	High rate of substitution; low conservation.
8. Population Effect	Maintains genetic uniformity within species.	Creates genetic diversity within and between species.
9. Outcome in Phylogeny	Short branches; close similarity in phylogenetic trees.	Long branches; distant relationships in phylogenetic trees.
10. Role in Evolution	Maintains existing functions; prevents excessive change.	Promotes speciation, adaptation and evolutionary innovation.

4. MOLECULAR DRIVE: KEY POINTS

- ✓ Maintains stability of essential genes.
- ✓ Removes harmful or unfavorable mutations.
- ✓ Ensures accurate transmission of genetic information.
- ✓ Common in genes with vital cellular functions.
- ✓ Observed in highly conserved sequences across species.

5. MOLECULAR DIVERGENCE: KEY POINTS

- ✓ Generates diversity at molecular level.
- ✓ Drives adaptation to new environments.
- ✓ May result from mutation, recombination, gene duplication, genetic drift.
- ✓ Leads to new gene functions and novel phenotypes.
- ✓ Important in evolution of new species.

6. FACTORS AFFECTING DIVERGENCE

- Point mutations
- Insertions / deletions
- Gene duplication
- Recombination
- Natural selection
- Genetic drift
- Geographical isolation
- Environmental differences

7. EXAMPLES

Drive (Conserved)

- Histone proteins
- Ribosomal RNA
- Glycolytic enzymes
- Actin, Tubulin
- DNA polymerase

Divergence (Variable)

- Immunoglobulin genes
- Hemoglobin (α vs β chains)
- MHC genes
- Receptor proteins
- Sperm proteins

8. SUMMARY TABLE

Parameter	Molecular Drive	Molecular Divergence
Trend	Similarity	Difference
Selection	Stabilizing	Diversifying / Other
Variation	Reduced	Increased
Conservation	High	Low
Evolutionary Role	Conservation	Innovation & Change

9. KEY POINTS TO REMEMBER

- Molecular drive = similarity (conservation).
- Molecular divergence = difference (variation).
- Drive reduces variation; divergence increases variation.
- Drive is due to stabilizing selection; divergence due to various evolutionary forces.
- Both are essential and complementary in evolution.

10. IN SHORT

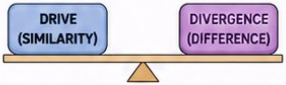
Molecular drive acts to preserve and maintain similarity in essential genes, while molecular divergence promotes differences that lead to diversity, adaptation and new species.

MEMORY TRICK

"Drive keeps alive, Divergence makes thrive!"

Drive = Conserves
↓
Similarity

Divergence = Diversifies
↓
Difference



SHORT NOTES

(a) DIVERGENCE OF TRANSCRIPTION SYSTEM IN BACTERIA AND ARCHAEA

Although bacteria and archaea are both prokaryotes, their transcription machineries differ significantly in composition, structure and function, reflecting their evolutionary divergence.

1. COMPARATIVE OVERVIEW

Feature	Bacteria	Archaea
RNA Polymerase	Single RNA polymerase (core: $\alpha_2\beta\beta'\omega$)	Multiple RNA polymerases (core: 8–14 subunits, homo/hetero-oligomeric)
Subunit Composition	4–5 subunits	More complex (similar to eukaryotic Pol II)
Promoters	−35 (TTGACA) and −10 (TATAAT) elements	TATA box (TATAWA) at ~25–30 bp upstream
Transcription Factors	σ (sigma) factors initiate transcription	TBP (TATA-binding protein), TFB and other factors (similar to eukaryotes)
Termination	Rho-dependent or Rho-independent	Rho-dependent only (so far known)
Chromatin Association	No histone-like proteins	Histone-like proteins bind DNA and influence transcription
Sensitivity to Antibiotics	Sensitive to rifampicin (targets β subunit)	Naturally resistant to rifampicin
Evolutionary Affinity	Closer to eukaryotic transcription system	Shares features with eukaryotes, indicating early divergence

2. KEY POINTS

- ✓ Archaeal RNA polymerase is more complex and eukaryote-like.
- ✓ Promoter recognition and transcription initiation differ significantly.
- ✓ These differences reflect adaptation to distinct cellular environments and evolutionary pathways.
- ✓ The divergence supports the view that Bacteria and Archaea evolved from a common ancestor but followed separate lines.

3. SIGNIFICANCE

- ★ Useful in understanding the evolution of gene expression machinery.
- ★ Helps in phylogenetic studies.
- ★ Antibiotic targets in bacteria (due to structural differences).

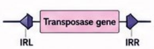
In summary: Bacterial transcription system is simpler and sigma factor–dependent, whereas archaeal system is more complex, TATA box–driven and eukaryote-like.

(b) ROLE OF TRANSPOSABLE ELEMENTS IN BACTERIAL EVOLUTION

Transposable elements (TEs) are DNA sequences that can move or copy themselves to new locations in the genome. They play a major role in shaping bacterial genomes and driving evolution.

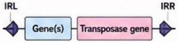
1. MAJOR TYPES OF TRANSPOSABLE ELEMENTS IN BACTERIA

Insertion Sequences (IS)



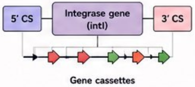
- Simplest TEs; contain only a transposase gene.
- Bounded by inverted repeats (IR).
- Move via "cut and paste" mechanism.

Transposons



- Carry additional genes (e.g., antibiotic resistance).
- Flanked by IS elements.
- Move as a unit.

Integrons and Gene Cassettes



- Capture and express gene cassettes.
- Important in adaptation, especially antibiotic resistance.

2. CONTRIBUTION TO BACTERIAL EVOLUTION

1. Generation of Genetic Diversity	TEs create mutations by insertion, deletion or gene disruption, leading to new traits.
2. Horizontal Gene Transfer (HGT)	Transposons and integrons mobilize genes between plasmids, chromosomes and species.
3. Spread of Antibiotic Resistance	Many resistance genes are carried by TEs, facilitating rapid dissemination in bacterial populations.
4. Genome Rearrangement	TEs cause inversions, duplications, deletions and translocations, reshaping genomes.
5. Regulation of Gene Expression	TE insertion near genes can alter their expression by providing new promoters or terminators.
6. Adaptation to Environment	By promoting genetic innovation and acquisition of beneficial genes, TEs help bacteria adapt to stress, toxins, and new niches.

3. EXAMPLES

- Tn3 family transposons carry antibiotic resistance genes.
- IS elements (e.g., IS1, IS10) are abundant in bacterial genomes.
- Integrons in *Vibrio*, *Pseudomonas*, and *Enterobacteriaceae* contribute to multidrug resistance.

4. KEY POINTS

- ★ TEs are powerful agents of genome plasticity.
- ★ They accelerate evolution and adaptation.
- ★ They can be beneficial (innovation) or harmful (gene disruption, instability).

In summary: Transposable elements drive bacterial evolution by generating genetic diversity, facilitating horizontal gene transfer, spreading adaptive traits and reshaping genomes.

GENETIC DRIFT

What is Genetic Drift?

Genetic drift is the random change in the frequency of alleles in a population from one generation to the next due to chance events.
It is not driven by natural selection.

Key Point

Chance, not choice, shapes allele frequencies.

1. KEY FEATURES

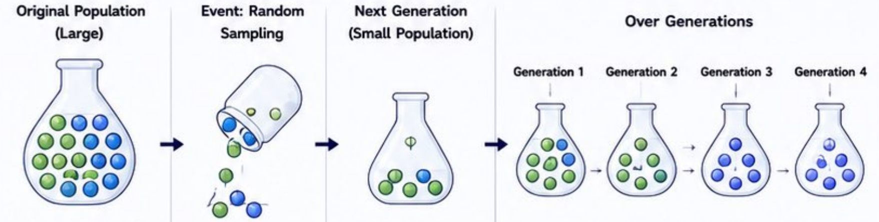
- Random process
- Affects allele frequencies in small populations more strongly
- Can lead to loss or fixation of alleles
- Reduces genetic variation
- Acts similarly on all alleles (not adaptive)

Allele Frequency Change by Chance (Not by Selection)

Chance events disturb the balance

2. HOW GENETIC DRIFT WORKS?

In a small population, chance events can change allele frequencies dramatically.



Original Population (Large)

● A allele ● a allele

Both alleles present in stable frequencies.

Event: Random Sampling

A few individuals by chance start a new population.

Next Generation (Small Population)

Allele frequencies change due to chance, not selection.

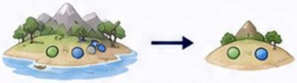
Over Generations

Generation 1 → Generation 2 → Generation 3 → Generation 4

Alleles may become less common and disappear, or become more common and get fixed.

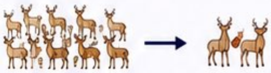
3. TYPES / FORMS

Founder Effect



A new population is formed by a few individuals. Their allele frequencies may differ from the original population.

Bottleneck Effect



A population size is drastically reduced due to a disaster (e.g., flood, fire, disease). The survivors may have different allele frequencies.

4. SIGNIFICANCE IN EVOLUTION

1. **Source of Evolutionary Change**
   It changes allele frequencies randomly, introducing variation on which natural selection can act.
2. **Loss of Genetic Variation**
   May lead to loss of alleles, reducing genetic diversity within populations.
3. **Differentiation of Populations**
   Different populations drift in different directions, leading to divergence and speciation over time.
4. **Important in Small Populations**
   In small or isolated populations, drift can overpower natural selection.
5. **Fixation of Neutral or Deleterious Alleles**
   Even alleles that are neutral or slightly harmful can become fixed by chance.

5. EXAMPLES

- Color of flowers in small, isolated plant populations.
- Variation in beak size in small bird populations on islands.
- Differences between isolated populations of the same species (e.g., Darwin's finches).
- Founder populations like Amish groups show genetic traits uncommon in the original large population.

6. LIMITATIONS

- Not a creative force; it acts randomly.
- Cannot produce adaptive changes directly.
- More effective in small populations, less in large populations.

7. COMPARISON: DRIFT vs SELECTION

Feature	Genetic Drift	Natural Selection
Cause	Chance events	Environmental pressure
Direction	Random	Non-random (adaptive)
Effect on Fitness	May reduce fitness	Increases fitness
Acts on	All alleles equally	Favorable alleles
More powerful in	Small populations	Large populations

8. CONDITIONS FAVORING GENETIC DRIFT

- Small population size
- Geographic isolation
- Sudden reduction in population size (bottleneck)
- Founder events

9. KEY TAKEAWAY

- ✓ Genetic drift is a random process.
- ✓ It is a powerful evolutionary force in small populations.
- ✓ It reduces genetic variation but can lead to fixation of alleles.
- ✓ It contributes to evolution by causing divergence and speciation.

IN SHORT

Genetic drift = Random change in allele frequencies. → Important in small populations → Leads to loss or fixation of alleles → Drives evolution over time.

Chance today, Evolution tomorrow.

Gemmata sp.

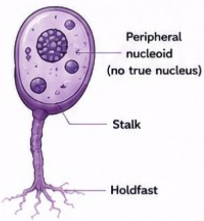
GEMMATA sp. AND GIARDIA sp.

CONNECTING LINKS BETWEEN PROKARYOTES AND EUKARYOTES

Giardia sp.

Both Gemmata sp. (a planctomycete bacterium) and Giardia sp. (a primitive eukaryotic protozoan) show features intermediate between prokaryotes and typical eukaryotes, hence considered as **connecting links** in evolution.

1. GEMMATA sp. (A PLANCTOMYCETE BACTERIUM)



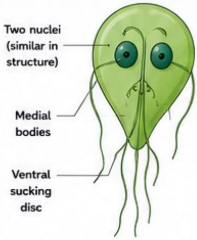
Salient Features

- Cell wall lacks peptidoglycan (unique among bacteria); instead contains glycoproteins.
- Intracytoplasmic membrane system (vesicles, tubules) present.
- DNA is in a nucleoid but is organized and associated with membrane.
- Ribosomes are 70S (prokaryotic type).
- Undergo budding reproduction – daughter cells arise as buds.
- Some species show gliding motility.

Intermediate Nature

Absence of peptidoglycan and presence of internal membrane system resemble eukaryotes, while 70S ribosomes, nucleoid and lack of true nucleus are prokaryotic.

2. GIARDIA sp. (A PRIMITIVE EUKARYOTIC PROTOZOAN)



Salient Features

- Two nuclei, but without true nuclear membrane and nucleolus.
- No mitochondria, Golgi body, ER or peroxisomes.
- Cytoskeletal elements (axonemes) similar to some bacteria.
- Hydrogenosomes present (anaerobic energy organelles; considered primitive to mitochondria).
- Reproduces by binary fission.
- Flagella typical of eukaryotes (9+2 axoneme).

Intermediate Nature

Presence of nuclei, flagella and cytoskeleton are eukaryotic, while absence of typical membrane-bound organelles and presence of hydrogenosomes resemble prokaryotes.

3. SIGNIFICANCE AS CONNECTING LINKS

1. Structural Continuity

Both show a mosaic of prokaryotic and eukaryotic characters, indicating gradual evolution from simple to complex forms.

2. Evolution of Cellular Organization

Gemmata shows early evolution of internal membrane systems; Giardia shows early evolution of nucleus and cytoskeletal organization.

3. Support Endosymbiotic Theory

Features like internal membranes in Gemmata and hydrogenosomes in Giardia suggest steps toward the origin of mitochondria and other organelles.

4. Bridge in Phylogeny

They occupy intermediate positions between prokaryotes and higher eukaryotes in molecular phylogenetic trees.

5. Evolution of Reproduction

Budding in Gemmata and binary fission in Giardia represent transition from asexual bacterial reproduction to eukaryotic cell division.

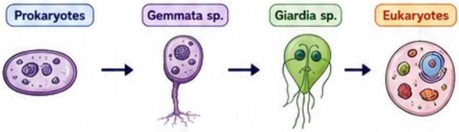
6. Insight into Early Life

Studying them helps reconstruct possible characteristics of the last common ancestor (LUCA) and early evolutionary pathways.

4. COMPARISON SUMMARY

Feature	Prokaryotes (Typical Bacteria)	Gemmata sp.	Giardia sp.	Eukaryotes (Typical)
Cell Wall	Peptidoglycan present	No peptidoglycan; glycoprotein cell wall	No cell wall	Cell wall (if present) of cellulose/chitin
Nucleus	Absent (nucleoid)	Nucleoid, but DNA associated with internal membranes	Two nuclei, but without nuclear membrane	True nucleus with nuclear membrane and nucleolus
Membrane-bound Organelles	Absent	Intracytoplasmic membrane system present	Absent (no mitochondria, Golgi, ER)	Present (mitochondria, ER, Golgi, lysosomes, etc.)
Ribosomes	70S	70S	70S	80S (cytoplasmic)
Energy Organelles	Absent	Absent	Hydrogenosomes present	Mitochondria present
Cytoskeleton	Simple (if present)	Simple elements	Cytoskeletal elements (axonemes, microtubules)	Well developed
Reproduction	Binary fission	Budding	Binary fission	Mitosis / Meiosis
Motility	Flagella (simple)	Gliding motility (some species)	Flagella (9+2 axoneme)	Cilia / Flagella (9+2 axoneme)
Evolutionary Position	Basal	Intermediate	Intermediate	Advanced

5. HOW THEY CONNECT PROKARYOTES AND EUKARYOTES



They represent evolutionary stepping stones from simple prokaryotic cells to complex eukaryotic cells.

6. KEY TAKEAWAY

- ✓ Gemmata sp. combines bacterial simplicity with eukaryote-like internal membranes and cell wall composition.
- ✓ Giardia sp. combines eukaryote-like nuclei and flagella with absence of typical organelles and presence of hydrogenosomes.
- ✓ Both provide vital evidence for gradual evolution and support the concept of common ancestry of life.
- ✓ Hence, they are considered important connecting links between prokaryotes and eukaryotes.

IN SHORT: Gemmata sp. (a unique bacterium) and Giardia sp. (a primitive eukaryote) show combinations of prokaryotic and eukaryotic characters, which help scientists understand the evolutionary transition from simple prokaryotes to complex eukaryotes.

HOW DOES ALPHA TAXONOMY DIFFER FROM BETA AND GAMMA TAXONOMY?

Roger R. Sneath proposed a polyphasic approach to bacterial taxonomy comprising three complementary levels: Alpha, Beta and Gamma taxonomy.

1. ALPHA TAXONOMY
(Phenotypic/Experimental)

Deals with the classification of organisms based on observable phenotypic characteristics.

2. BETA TAXONOMY
(Genotypic/Comparative)

Deals with the classification based on overall genomic similarity and relatedness.

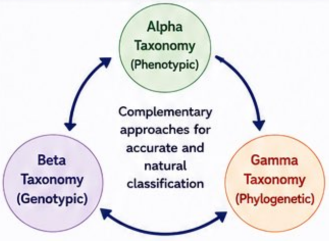
3. GAMMA TAXONOMY
(Phylogenetic/Evolutionary)

Deals with classification based on evolutionary relationships and phylogenetic lineages.

4. KEY DIFFERENCES AT A GLANCE

Feature	Alpha Taxonomy	Beta Taxonomy	Gamma Taxonomy
Basis	Phenotypic characters (morphological, physiological, biochemical, chemotaxonomic)	Genotypic characters (DNA–DNA hybridization, G+C content, genomic data)	Phylogenetic/evolutionary information (16S rRNA sequences, whole genome phylogeny)
Approach	Experimental observation and characterization	Comparative analysis of genomic relatedness	Inference of evolutionary relationships
Data Type	Phenotypic data	Genotypic (molecular) data	Phylogenetic (evolutionary) data
Level of Relatedness Revealed	Shows similarity based on expressed traits; may include unrelated organisms	Shows overall genetic similarity; groups genomes with high relatedness	Shows evolutionary lineage and common ancestry
Resolution	Low to moderate	Higher than alpha	Highest (deep evolutionary resolution)
Tools/Methods	Microscopy, culture characteristics, biochemical tests, API, fatty acids, etc.	DNA–DNA hybridization, G+C content, DNA homology, genome sequencing, ANI	16S rRNA sequencing, multigene/whole genome phylogenetic analysis
Main Objective	Identification and classification of isolates	Grouping into genomic species and higher taxa	Understanding evolutionary relationships and natural classification
Taxonomic Output	Species description, phenotypic species, uubspecies, biovars	Genomic species (GGSP), genomospecies clusters	Phylogenetic taxa (clades, lineages, orders, etc.)
Strengths	Simple, cost-effective, useful for identification in routine labs	More objective, less affected by environment, reveals hidden relationships	Reflects true evolutionary history, most informative for classification
Limitations	Affected by environment, phenotypic plasticity; may group unrelated organisms	Does not always indicate evolutionary direction; requires good quality DNA	More complex, requires bioinformatics and robust phylogenetic data
Example	Identification of *E. coli* based on biochemical tests and colony morphology	Grouping of bacterial strains with ≥ 70% DNA–DNA relatedness	Placement of bacteria in a phylogenetic tree based on 16S rRNA gene sequences

5. HOW THEY ARE RELATED?


Alpha Taxonomy (Phenotypic)
Beta Taxonomy (Genotypic)
Gamma Taxonomy (Phylogenetic)

Complementary approaches for accurate and natural classification

6. IN SHORT

- ✓ Alpha taxonomy uses phenotype (what it looks and behaves like).
- ✓ Beta taxonomy uses genome similarity (what genes it has).
- ✓ Gamma taxonomy uses evolution (where it came from and how it evolved).

★ Together, they provide a polyphasic and robust framework for modern microbial taxonomy.

7. SUMMARY COMPARISON

Alpha = "Phenotype"	What it is like (observable features)
Beta = "Genotype"	What it has (genomic composition)
Gamma = "Phylogeny"	Where it fits (evolutionary history)

★ **Alpha, Beta and Gamma taxonomy represent a polyphasic approach—combining phenotype, genotype and phylogeny—to achieve natural, meaningful and stable classification of microorganisms.**

THEORIES OF BIOLOGICAL CLASSIFICATION

Different theories explain how organisms are grouped based on similarities and differences.

1. MAJOR THEORIES

1. ARTIFICIAL CLASSIFICATION

Proposed by: Aristotle, Theophrastus (Ancient Greece)

The earliest attempt to group organisms using easily observable characters.

Basis of classification

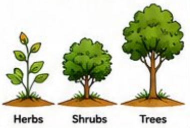
- Gross morphological characters (habitat, size, shape, usefulness)

Key features

- Simple and convenient
- Based on few characters
- Did not reflect natural relationships

Example/Outcome

Plants were grouped as herbs, shrubs and trees.



2. NATURAL CLASSIFICATION

Proposed by: J.B. Lamarck, A.P. de Candolle (18th–19th C.)

Organisms are grouped based on many natural characters showing real affinities.

Basis of classification

- Many morphological, anatomical and physiological characters

Key features

- Used many characters
- Reflected natural relationships to some extent
- Did not explain evolutionary relationships

Example/Outcome

De Candolle's natural system of plants (based on overall similarity).

3. PHYLOGENETIC CLASSIFICATION

Proposed by: Ernst Haeckel (1866)

Classification based on evolutionary relationships and descent with modification.

Basis of classification

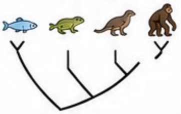
- Phylogeny (evolutionary history)

Key features

- Uses both similarities and differences
- Emphasizes common ancestry
- Introduced the concept of phylogenetic tree"

Example/Outcome

Organisms are arranged on a tree showing evolutionary relationships.



4. EVOLUTIONARY CLASSIFICATION

Proposed by: Julian Huxley, G.G. Simpson (20th C.)

An advanced version of phylogenetic classification incorporating modern evolutionary concepts.

Basis of classification

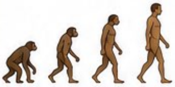
- Evolutionary relationships
- Genetic, paleontological, biochemical and cytological evidence

Key features

- Integrates multiple lines of evidence
- Recognizes evolutionary lineages and natural groups (clades)
- More objective and predictive

Example/Outcome

Basis of modern taxonomy and systematics.



5. NUMERICAL (PHENETIC) CLASSIFICATION

Proposed by: R.R. Sokal & P.H.A. Sneath (1963)

Organisms are grouped based on overall similarity using numerical methods.

Basis of classification

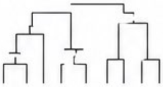
- Overall phenetic similarity (many characters given equal weight)

Key features

- Uses statistical methods and computer
- No emphasis on evolution
- Produces phenograms (similarity trees)

Example/Outcome

Used widely in microbial classification.



2. COMPARISON OF THEORIES

Feature	Artificial	Natural	Phylogenetic	Evolutionary	Numerical (Phenetic)
Time period	Ancient times	18th–19th century	19th century	20th century	Mid 20th century
Basis	Few external characters	Many natural characters	Evolutionary descent	Evolution + multiple evidence	Overall similarity (phenetic)
Nature of approach	Subjective	More natural, still subjective	Evolutionary, hypothetical	Evolutionary, scientific & objective	Non-evolutionary, statistical
Use of evolution	No	No	Yes (descent with modification)	Yes (strongly emphasized)	No
Type of data	Morphology	Morphology, anatomy, physiology	Morphology, embryology, paleontology	Molecular, genetic, cytological, fossil, etc.	Many characters, equal weight
Output	Artificial groups	Natural groups	Phylogenetic tree	Natural groups (clades, lineages)	Phenogram (similarity tree)
Limitation	Very artificial, ignores relationships	Does not show evolutionary lines	Limited data available	Complex, data intensive	Ignores evolution, equal weight to all characters
Use today	Obsolete	Of historical importance	Still used in phylogeny	Basis of modern classification	Used in numerical taxonomy

3. IMPORTANCE OF THESE THEORIES

- Helped in understanding diversity and relationships among organisms.
- Provided a historical framework for the development of taxonomy.
- Evolutionary and numerical approaches laid the foundation for modern molecular systematics.
- Modern classification integrates phylogeny with molecular data (Genomics, Proteomics, etc.).
- Essential for biodiversity conservation, ecology and biotechnology.

4. SUMMARY – EVOLUTION OF CLASSIFICATION THOUGHT

Artificial

Based on few, easily observable traits.

→

Natural

Based on many natural characters; more realistic.

→

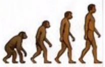
Phylogenetic

Based on evolution and common ancestry.

→

Evolutionary

Integrates multiple evidences; forms natural groups (clades).



→

Numerical

Based on overall similarity using statistical methods.

From simplicity to complexity – from form to function to evolution and molecules

5. IN SHORT

- ✓ Artificial – based on few observable characters.
- ✓ Natural – based on many natural characters.
- ✓ Phylogenetic – based on evolutionary descent ("tree of life").
- ✓ Evolutionary – uses all available evidence to understand evolution.
- ✓ Numerical – based on overall similarity using statistical methods.

Modern taxonomy is a synthesis of evolutionary and numerical approaches supported by molecular data.

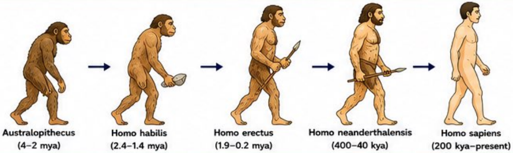
In conclusion: Each theory contributed to our understanding of life's diversity. From artificial groupings to modern molecular phylogenetics, the goal remains the same – to reflect natural relationships and evolutionary history in classification.

DESCRIBE THE FOLLOWING (5 × 2 = 10 MARKS)

(a) TRENDS IN GENERAL MORPHOLOGY DURING HUMAN EVOLUTION

Human evolution shows gradual changes in body size, posture, skull, brain, dentition and limbs, reflecting adaptation to bipedalism, tool use and complex life.

1. MAJOR TRENDS



Feature	Australopithecus	Homo habilis	Homo erectus	Homo neanderthalensis	Homo sapiens
Posture & Locomotion	Bipedal, stooped posture	More upright bipedal	Fully upright bipedal	Fully upright, robust build	Fully upright, gracious, endurance walking/running
Body size	Small (90–110 cm)	Slight increase	Taller (150–170 cm)	Robust, muscular	Variable, slender build
Skull capacity	~400–550 cc	~600–700 cc	~800–1100 cc	~1200–1600 cc	~1200–1600 cc
Cranial features	Small braincase, prognathous face	Less prognathism, thicker skull	Low forehead, thick brow ridges	Long, low skull, occipital bun	High forehead, round skull, chin present
Face & jaws	Prognathous, large jaws	Reduced prognathism	Reduced jaws, less prognathism	Mid-face projection	Orthognathous face, chin
Dentition	Large canines, diode (U-shaped) arch	Reduced canines, parabolic arch	Further reduced teeth	Worn teeth, large molars	Small teeth, parabolic arch
Limbs	Arms longer than legs	Arms shorter than legs	Modern human proportions begin	Short, strong limbs	Long legs, short arms
Hands	Strong, curved fingers	Better precision grip	Good precision grip	Strong, broad hands	Highly skilled hands
Other features	Body hair abundant	Used simple tools	Tool-making, controlled fire	Burials, culture, clothing	Complex language, culture, art, technology

2. SUMMARY

✓ Trends show increase in brain size, reduction in prognathism and jaws, development of chin, change to parabolic dentition, modern limb proportions and specialization of hands, with complete bipedalism.

(b) SECONDARY AND TERTIARY ENDOSYMBIOSIS

Endosymbiosis is the incorporation of one cell (endosymbiont) within another (host cell). Beyond the primary event (origin of mitochondria and plastids), additional events led to diversity in eukaryotes.

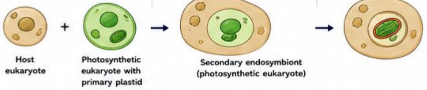
A. SECONDARY ENDOSYMBIOSIS

A eukaryotic cell engulfs another eukaryotic cell that already contains primary endosymbionts (a plastid).

Step 1 A non-photosynthetic eukaryote engulfs a photosynthetic eukaryote.

Step 2 The engulfed cell is retained and becomes an endosymbiont.

Step 3 Over time, the endosymbiont is reduced to a secondary plastid (complex plastid).


Host eukaryote
+
Photosynthetic eukaryote with primary plastid
Secondary endosymbiont (photosynthetic eukaryote)

Examples

- Dinoflagellates
- Diatoms
- Brown algae
- Euglenids

Key features

- ◆ Plastid has 3 or 4 surrounding membranes (due to engulfment of a eukaryote).
- ◆ Nucleus of endosymbiont is lost; genes transferred to host nucleus.

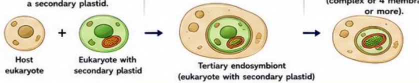
B. TERTIARY ENDOSYMBIOSIS

A eukaryote engulfs another eukaryote that itself contains a secondary plastid.

Step 1 A eukaryote engulfs a eukaryote that has a secondary plastid.

Step 2 Engulfed cell is retained as endosymbiont.

Step 3 Endosymbiont is reduced to a tertiary plastid (complex of 4 membranes or more).


Host eukaryote
+
Eukaryote with secondary plastid
Tertiary endosymbiont (eukaryote with secondary plastid)

Examples

- Certain dinoflagellates (e.g., some with tertiary plastids)
- Cryptophytes (through multiple events)

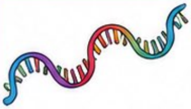
Key features

- ◆ Plastid has 4 or more membranes (additional membranes from engulfed eukaryote).
- ◆ Occurs in some lineages leading to great diversity of algae.

3. SIGNIFICANCE

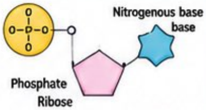
- Explains diversity of plastids in algae (different pigments, membranes).
- Shows repeated endosymbiotic events shaping eukaryotic evolution.
- Important in evolution of algal lineages and ecological adaptations.
- Supported by molecular phylogeny, organelle membrane structure and gene transfer.

IN SHORT: Human evolution shows gradual trends toward modern morphology and higher brain.
Secondary and tertiary endosymbiosis explain the origin of complex plastids in many eukaryotes.



RNA WORLD HYPOTHESIS

Life began with RNA – the first genetic material and catalyst



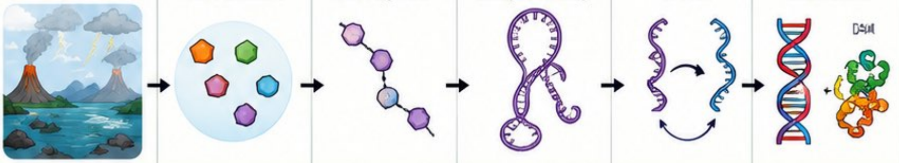
1. WHAT IS THE RNA WORLD HYPOTHESIS?

- Proposed by Cech (1986) and Gilbert (1986).
- Suggests that early life on Earth was based on RNA molecules before the evolution of DNA and proteins.
- RNA could store genetic information and catalyze chemical reactions.

2. WHY RNA?

- ✓ Stores genetic information (like DNA)
- ✓ Catalyzes reactions (like proteins – *ribozymes*)
- ✓ Single-stranded – can fold into complex 3-D structures
- ✓ Can self-replicate
- ✓ Chemically more stable than other early polymers

3. THE RNA WORLD: PROPOSED EVOLUTIONARY SEQUENCE



① **Prebiotic Soup** (~4.5 billion years ago)
Simple inorganic molecules (CH_3, NH_3, H_2O, CO_2, H_2S, PO_3^{3-}, etc.) present in the early Earth environment.

② **Formation of RNA Monomers**
Ribose, phosphate and nitrogenous bases combine to form ribonucleotides.

③ **Formation of RNA Polymers**
Ribonucleotides polymerize (on clay surfaces, tidal pools, or ice matrices) to form RNA strands.

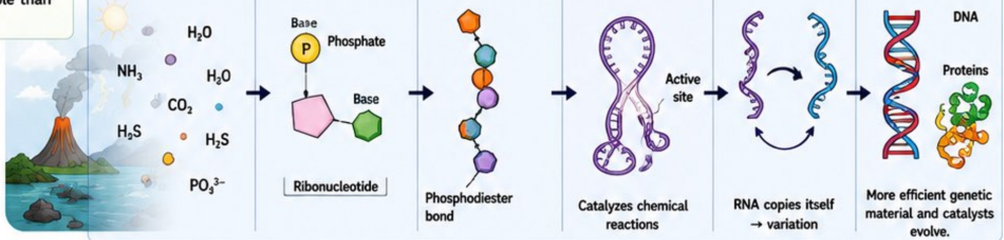
④ **RNA Molecules with Catalytic Activity**
Some RNA molecules act as ribozymes and catalyze reactions (peptide bond formation, etc.).

⑤ **Self-Replication of RNA**
RNA molecules replicate with imperfect fidelity → variation arises.

⑥ **Evolution of DNA and Proteins**
Eventually, DNA (more stable) took over genetic storage and proteins became the main catalysts.

4. WELL LABELLED DIAGRAM: THE RNA WORLD HYPOTHESIS

Simple Inorganic Molecules → **Ribonucleotides (Building blocks)** → **RNA Polymer Formation** → **RNA with Catalytic Activity (Ribozymes)** → **Self-Replication of RNA** → **Emergence of DNA and Proteins**



Catalyzes chemical reactions

RNA copies itself → variation

More efficient genetic material and catalysts evolve.

5. EVIDENCE IN SUPPORT

- ◆ Ribozymes exist today (e.g., RNA in ribosome, self-splicing introns).
- ◆ RNA can self-replicate in laboratory (template-directed synthesis).
- ◆ All living cells use RNA in central dogma (DNA → RNA → Protein).
- ◆ Simplicity of RNA compared to proteins and DNA.

6. IMPORTANCE

- ✓ Explains the origin of life from simple molecules.
- ✓ Provides a natural link between non-living chemistry and living systems.
- ✓ RNA could perform both information storage and catalysis before specialization evolved.
- ✓ Supported by modern discoveries of ribozymes.

7. LIMITATIONS

- ⊗ RNA is less stable than DNA.
- ⊗ Prebiotic synthesis of ribonucleotides is difficult.
- ⊗ Self-replication of long RNA strands is not fully efficient.
- ⊗ Transition from RNA to DNA-protein world is not completely explained.

8. KEY POINTS TO REMEMBER

- ★ RNA was the first biomolecule of life.
- ★ RNA can store genetic information and catalyze reactions.
- ★ Life started as an RNA-based system (RNA World).
- ★ Later, DNA evolved for stability and proteins for efficiency.
- ★ All life today is a product of this evolutionary transition.

9. ONE LINE SUMMARY

"The RNA World Hypothesis proposes that early life was based on RNA molecules which could store genetic information and catalyze reactions, before the evolution of DNA and proteins."

10. IN SHORT

The RNA world hypothesis suggests that life on Earth began with RNA molecules that could both store genetic information and catalyze chemical reactions. These RNA molecules self-replicated and evolved. Later, DNA replaced RNA as genetic material for stability, and proteins became the main catalysts.

MEMORY TRICK

"RNA First, Life First"
(RNA came first and made life first)

R – Ribozyme **N** – Nucleic acid **A** – Ancient molecule